

PCT

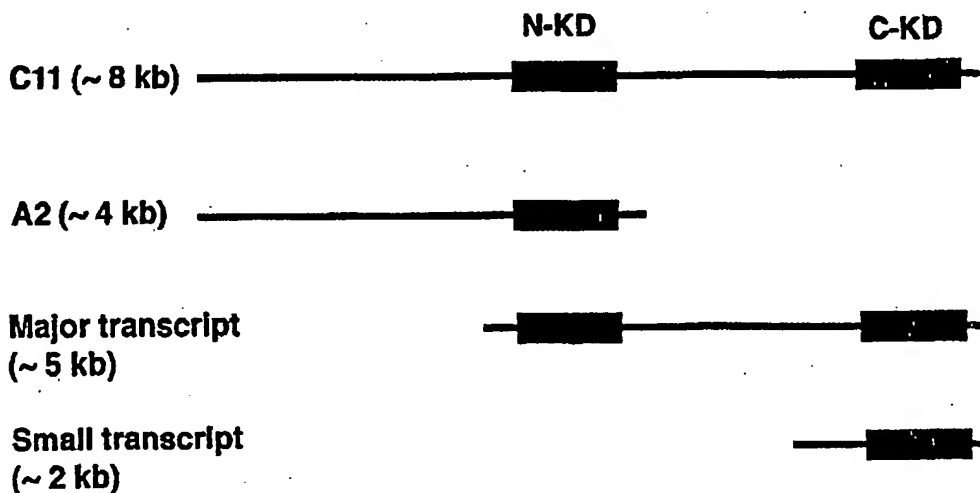
WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, C07K 14/47, 16/18, C12N 15/11, G01N 33/68, A61K 38/17, 39/395, 48/00		A1	(11) International Publication Number: WO 00/63381
			(43) International Publication Date: 26 October 2000 (26.10.00)
(21) International Application Number: PCT/US00/09488		(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), DM, DZ, EE, EE (Utility model), ES, FI, FI (Utility model), GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 11 April 2000 (11.04.00)			
(30) Priority Data: 60/129,553 16 April 1999 (16.04.99) US			
(71) Applicant (for all designated States except US): SCIOS, INC. [US/US]; 820 West Maude Avenue, Sunnyvale, CA 94086 (US).			
(72) Inventors; and (75) Inventors/Applicants (for US only): ZENG, Wenlin [CN/US]; 2210 Rock Street #24, Mountain View, CA 94043 (US). STANTON, Lawrence [US/US]; 73 Turnsworth Avenue, Redwood City, CA 94062 (US). KONG, Haiyan [CN/US]; Apartment #6, 914 Tamarack Lane, Sunnyvale, CA 94086 (US).			
(74) Agent: ALTMAN, Daniel, E.; Knobbe, Martens, Olson and Bear, LLP, 16th Floor, 620 Newport Center Drive, Newport Beach, CA 92660 (US).		Published With international search report.	

(54) Title: MAMMALIAN PROTEIN WITH PUTATIVE FUNCTION IN SIGNAL TRANSDUCTION

Splicing Variants of h19G5



(57) Abstract

Polypeptides capable of regulating signal transduction, which preferably exhibit kinase activity, or antibodies against such polypeptides that inhibit the interaction of these polypeptides with other mediators of signal transduction, may be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammalian hosts. In addition, these polypeptides can facilitate the identification or isolation of additional mediators of signal transduction associated with disease, preferably cardiac disease, which in turn may also be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammals.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

MAMMALIAN PROTEIN WITH PUTATIVE FUNCTION IN SIGNAL TRANSDUCTION

FIELD OF THE INVENTION

5 The present invention relates to compounds and methods for the identification, prevention or treatment of disease, preferably cardiac disease, in a mammal through the administration of polypeptides capable of regulating signal transduction, which preferably exhibit kinase activity, or antibodies against such polypeptides that inhibit the interaction of these polypeptides with other mediators of signal transduction. In addition, the compounds and methods of the present invention can facilitate the identification or isolation of additional mediators of signal transduction
10 associated with disease, preferably cardiac disease, which in turn may also be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammals.

BACKGROUND OF THE INVENTION

 Certain biological functions, such as growth and differentiation, are tightly regulated by signal transduction
15 pathways within cells. Signal transduction pathways maintain the balanced steady state functioning of a cell. Disease states can arise when signal transduction in a cell breaks down, thereby removing the control that typically exists over cellular functions. Because signal transduction networks regulate a multitude of cellular functions depending upon the cell type, a wide variety of diseases can result from abnormalities in such networks. Devastating diseases such as cancer, autoimmune diseases, allergic reactions, inflammation, neurological disorders and hormone-related diseases can
20 result from abnormal signal transduction. For example, tumors may develop when regulation of cell growth is disrupted.

 Despite a long-felt need to understand and discover methods for regulating cells involved in various disease states, the complexity of signal transduction pathways has precluded the development of products and processes for regulating cellular function by manipulating signal transduction pathways in a cell. As such, there remains a need for
25 products and processes that permit the implementation of predictable controls of signal transduction in cells, thus enabling the treatment of various diseases that are caused by abnormal cellular function.

 Such diseases may include cardiac diseases, which may include congestive heart failure (CHF), dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary
30 hypertension, arterial hypertension, renovascular hypertension, arteriosclerosis, atherosclerosis, and cardiac tumors. By way of example, CHF is a major cardiac disease associated with extensive morbidity and mortality. Approximately five million individuals in the United States suffer from some form of CHF. Traditionally, treatment of CHF occurs by a series of agents including diuretics, vasodilators, angiotensin converting enzyme inhibitors, β -adrenergic antagonists, and positive inotropes like digoxin. These drugs, however, principally provide symptomatic relief and typically only
35 extend the life of one suffering from the disease for periods ranging from 6-12 months.

The pathophysiology of CHF is rather complex. Generally, the central hallmark of the disease is the inability of the heart to pump sufficient oxygenated blood to meet the demands of peripheral tissues. Numerous etiologies contribute to the development of CHF, including primary diseases of, or insults to, the myocardium itself, cardiac defects, hypertension, inflammation, kidney disease and vascular disease. These conditions lead to the hypertrophy and remodeling of the cardiac ventricles which, if unchecked, ultimately reduce the mechanical performance of the heart. Forces associated with the inability of the heart to pump blood ultimately lead to the release of neurohormones like catecholamines, renin-angiotensin, aldosterone, endothelin and related factors into the circulation. Elevations in plasma levels of many of these circulating neurohormones have a deleterious impact on the outcome of patients with CHF. Local production of these neurohormonal factors in the heart is believed to contribute centrally to the disease. Thus, an important therapeutic strategy has been to block this neurohormonal axis contributing to the pathogenesis of this disease.

Factors known to contribute centrally to the pathophysiology of heart disease are biosynthesized in the heart itself. These factors are produced in cardiac myocytes, fibroblasts, smooth muscle and endothelial cells, and inflammatory cells associated with the myocardium. For example, the heart contains its own renin-angiotensin system. Blockade of the cardiac renin-angiotensin system may contribute significantly to the therapeutic efficacy of the therapeutic class of agents known as angiotensin converting enzyme (ACE) inhibitors.

The heart also produces other factors including endothelins, bradykinin, adrenomedullin, tumor necrosis factor, transforming growth factors, and natriuretic peptides. Unfortunately, therapeutic strategies are limited to the modulation of such substances, which are already known to contribute to the disease. Indeed, the functional contributions of only a minor fraction of all known secreted factors encoded by the human genome have apparently been defined.

The foregoing shows a need for methods and products involving the prevention or treatment of disease in mammals involving the mediation of signal transduction. The administration of polypeptides capable of regulating signal transduction, which preferably exhibit kinase activity, or antibodies against such polypeptides that inhibit the interaction of these polypeptides with other mediators of signal transduction, in addition to the identification or isolation of additional mediators of signal transduction associated with disease, preferably cardiac disease, which in turn may also be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammals, can facilitate such prevention or treatment.

30

SUMMARY OF THE INVENTION

An objective of the present invention is therefore the prevention or treatment of disease, preferably cardiac disease, in mammals through the administration of polypeptides capable of regulating signal transduction, which preferably exhibit kinase activity, or antibodies against such polypeptides that inhibit the interaction of these polypeptides with other mediators of signal transduction, in addition to the identification or isolation of additional

mediators of signal transduction associated with disease, preferably cardiac disease, which in turn may also be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammals.

In accomplishing these and other objectives, the present invention preferably provides a purified polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating
5 signal transduction. In a preferred embodiment, the polypeptide is capable of catalyzing the transfer of a phosphate group from a donor molecule to an acceptor molecule.

In another embodiment, the present invention preferably provides an isolated DNA molecule encoding a purified polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction. The present invention may also preferably be an isolated DNA molecule
10 comprising the nucleotide sequence of SEQ ID NOS: 2, 3 or 5.

In yet another embodiment, the present invention preferably provides a vector comprising a DNA molecule encoding a purified polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction. In another aspect, the present invention provides a host cell transformed with such a vector. In one other embodiment, the present invention may preferably provide the above-
15 described transformed host cell, where the host cell produces a polypeptide capable of regulating signal transduction. In a preferred embodiment, the above-described transformed host cell produces a polypeptide capable of catalyzing the transfer of a phosphate group from a donor molecule to an acceptor molecule.

In another preferred embodiment, the present invention provides an isolated antibody against a polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating
20 signal transduction. In a preferred embodiment, the antibody is a monoclonal antibody. In another preferred embodiment, the antibody is capable of inhibiting the regulation of signal transduction. In yet another preferred embodiment, the antibody is capable of inhibiting the transfer of a phosphate group from a donor molecule to an acceptor molecule.

The present invention may also preferably provide an isolated nucleic acid capable of hybridizing under high stringency conditions to a DNA molecule comprising the nucleotide sequence of SEQ ID NOS: 2, 3 or 5. In a preferred
25 embodiment, this isolated nucleic acid is capable of inhibiting the regulation of signal transduction. In yet another preferred embodiment, this isolated nucleic acid is capable of inhibiting said transfer of said phosphate group from said donor molecule to said acceptor molecule.

In a preferred embodiment, the present invention provides a method of preventing or treating disease in a mammal comprising administering to said mammal an effective amount of material, selected from the group consisting
30 of the polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and the antibody against this polypeptide, in a pharmaceutically acceptable sterile vehicle. In a preferred embodiment, the mammal may be a human. In another, the disease may be cardiac disease.

The present invention may also preferably provide a vaccine for preventing disease in a mammal comprising administering to said mammal an effective amount of material, selected from the group consisting of the polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and the antibody against this polypeptide, in a pharmaceutically acceptable sterile vehicle. In a preferred embodiment, the mammal may be a human. In another, the disease may be cardiac disease.

In a preferred embodiment, the present invention provides a method of preventing or treating disease in a mammal comprising administering to said mammal syngeneic cells transformed with a vector comprising a DNA molecule encoding a purified polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and wherein the transformed syngeneic cells produce a polypeptide capable of regulating signal transduction. In a preferred embodiment, the mammal may be a human. In another, the disease may be cardiac disease.

The present invention may also preferably provide a method of preventing or treating disease in a mammal comprising administering to said mammal syngeneic cells transformed with a vector comprising a DNA molecule encoding a purified polypeptide comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and wherein the transformed syngeneic cells produce a polypeptide capable of catalyzing the transfer of a phosphate group from a donor molecule to an acceptor molecule. In a preferred embodiment, the mammal may be a human. In another, the disease may be cardiac disease.

In a preferred embodiment, the present invention may provide a kit for detecting the expression of a protein capable of regulating signal transduction, comprising a polypeptide, which comprises the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction. In a preferred embodiment, this kit further comprises a detectable label selected from the group consisting of colorimetric, enzymatic, chemiluminescent, fluorescent and radioactive labels.

In another preferred embodiment, the present invention may provide a kit for detecting the expression of a protein capable of acting as a donor molecule or an acceptor molecule of a phosphate group comprising a polypeptide, which comprises the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction. In a preferred embodiment, this kit further comprises a detectable label selected from the group consisting of colorimetric, enzymatic, chemiluminescent, fluorescent and radioactive labels.

The present invention may also preferably provide a method for detecting the expression of a protein capable of regulating signal transduction, comprising contacting a sample with a polypeptide, which comprises the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and detecting any effect of the sample on an indicator of signal transduction. In a preferred embodiment, the polypeptide is immobilized to a solid support. In another preferred embodiment, the phosphate group is detectably labeled.

In another preferred embodiment, the present invention may provide a method for detecting the expression of a protein capable of acting as a donor molecule or an acceptor molecule of a phosphate group, comprising contacting a

sample with a polypeptide, which comprises the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 wherein the polypeptide is capable of regulating signal transduction, and detecting any effect of the sample on an indicator of signal transduction, and detecting any transfer of the phosphate group. In a preferred embodiment, the polypeptide is immobilized to a solid support. In another preferred embodiment, the phosphate group is detectably labeled.

5 Other objectives, features, and advantages of the present invention will become apparent from the following detailed description. The detailed description and the specific examples, while indicating preferred embodiments of the invention, are provided by way of illustration only. Accordingly, the present invention also includes those various changes and modifications within the spirit and scope of the invention that may become apparent to those skilled in the art from this detailed description.

10

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 illustrates eight overlapping human cDNA clones of 19G5.

Figure 2 depicts homology alignment of amino acid sequences of human, rat and mouse clones corresponding to 19G5.

15 Figure 3 depicts the likely gene structure of human 19G5 (H19G5), which reveals at least 10 exons and 9 introns.

Figure 4 is a schematic diagram of four cDNA clones corresponding to splicing variants of H19G5. The longest clone (C11) contains two kinase domains, the N-terminal and the C-terminal kinase domains (N-KD and C-KD).

Figure 5 is a schematic diagram comparing the domain structure of 19G5 and Trio proteins.

20 Figure 6 is the sequence comparison of the kinase domains of H19G5 (N-terminal and C-terminal kinase domains), Trio, and smooth muscle myosin light chain (SM MLCK).

Figure 7 is the sequence comparison of the guanine nucleotide exchange factor (GEF) domains of H19G5 and Trio.

25 Figure 8 depicts a Northern blot analysis of various rat tissue samples using rat 19G5 DNA as a probe. Heart tissue reveals two transcripts (2 kb and a 4.4 kb) of R19G5. Multiple bands of weak hybridization are seen in skeletal muscle. Parallel Northern analysis of various rat tissue samples using a β -actin probe suggests approximate equal input of mRNA in various samples and integrity of mRNA.

30 Figure 9 depicts a Northern blot analysis of various human tissue samples using H19G5 DNA probe. Heart tissue reveals multiple transcripts (5 kb, 3 kb, 2.4 kb and 1.8 kb) derived from H19G5 gene. Skeletal muscle and brain tissues show multiple bands of weak hybridization.

Figure 10 depicts a Southern blot analysis of human genomic DNA using H19G5 DNA as a probe (SEQ ID NO: 2).

Figure 11 shows the subcellular localization of 19G5-GFP fusion proteins in mouse myoblast cell line C2C12. Three 19G5-GFP fusion protein expression constructs were made using three different 19G5 cDNA clones, the longest

human 19G5 clone C11 [h19G5(C11)-GFP], a 2.7 kb clone of human 19G5 containing the C-terminal kinase domain [h19G59F1)-GFP], and the rat 19G5 small transcript [r19G5(S)-GFP]. The control GFP vector and the 19G5-GFP fusion expression constructs were transfected into C2C12 cells. The 19G5-GFP fusion proteins' localization was detected using confocal microscopy.

5 Figure 12 shows that H19G5 protein expressed by the clone C11 binds to the small G protein Cdc42. The lysate of 293 EBNA cells transfected with H19G5-C11 expression construct was incubated with GST-Cdc42 immobilized on glutathione-agarose. After washing, the complex was resuspended in SDS sample buffer, boiled and run on a SDS-PAGE, and Western blotted with an anti-H19G5 monoclonal antibody.

10 Figure 13 shows phase contrast micrographs of C2C12 myoblasts undergoing differentiation into myotubes. Undifferentiated C2C12 cells are shown in Day 0. Differentiation of C2C12, induced by placing in 2% horse serum, is apparent on Day 3 and Day 5 as shown.

Figure 14 shows induction of myogenin protein expression when C2C12 myoblast cells are induced to differentiate into myotubes. Myogenin is a marker of myotubes.

Figure 15 shows induction of 19G5 RNA expression during the differentiation of myoblasts into myotubes.

15 Figure 16 shows inhibition of the induction of 19G5 expression by TFG- β during C2C12 differentiation.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Those skilled in the art will recognize that the products and methods embodied in the present invention may be applied to a variety of systems, constructed with various materials using various methods. Accordingly, the present invention is not limited to any particular environment, and the following description of specific embodiments of the present invention are for illustrative purposes only.

20 The present invention preferably provides methods for the prevention or treatment of disease, preferably cardiac disease, in mammals through the administration of polypeptides capable of regulating signal transduction, which preferably exhibit kinase activity, or antibodies against such polypeptides that inhibit the interaction of these polypeptides with other mediators of signal transduction, in addition to the identification or isolation of additional mediators of signal transduction associated with disease, preferably cardiac disease, which in turn may also be used in the identification, prevention or treatment of disease, preferably cardiac disease, in mammals. The cardiac diseases according to the present invention may include congestive heart failure (CHF), dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arterial hypertension, renovascular hypertension, arteriosclerosis, atherosclerosis, and cardiac tumors.

30 An embodiment of the invention is a purified polypeptide comprising an amino acid sequence having at least 95% sequence identity with the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9. As used herein, polypeptide refers to a linear series of amino acid residues connected to one another by peptide bonds between the alpha-amino

groups and carboxy groups of adjacent amino acid residues. Additional covalent bonds between portions of the peptide may also be present to restrain the conformation of the molecule, such as amide and disulfide bonds. When used herein, polypeptide also refers to a linear series of amino acid residues connected one to the other as in a peptide. The term synthetic peptide means a chemically derived chain of amino acid residues linked together by peptide bonds that is free of naturally occurring proteins and fragments thereof.

The one and three-letter symbols used to represent the amino acid residues in the polypeptides of the present invention are those symbols commonly used in the art. The amino acid residues are preferred to be in the L isomeric form. However, residues in the D isomeric form may be substituted for any L-amino acid, as long as the desired functional property of signal transduction mediation is retained by the peptide. The one and three-letter symbols used herein refer to the following amino acids: Ser (S) is serine; Ile (I) is isoleucine; Gln (Q) is glutamine; Phe (F) is phenylalanine; His (H) is histidine; Trp (W) is tryptophan; Lys (K) is lysine; Asn (N) is asparagine; Leu (L) is leucine; Gly (G) is glycine; Thr (T) is threonine; Asp (D) is aspartic acid; Arg (R) is arginine; and Ala (A) is alanine.

Polypeptides of the present invention include variants, fragments and chemical derivatives of the polypeptides comprising the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9 as long as they are capable of mediating signal transduction. Polypeptides thus may include soluble peptides, Ig-tailed fusion peptides (including immunoadhesions), members of random peptide libraries (*see, e.g., Lam, K.S. et al., Nature 354:82-84 (1991); Houghten, R. et al., Nature 354:84-86 (1991)*), combinatorial chemistry-derived molecular libraries made of D-and/or L-configuration amino acids, and phosphopeptides (including members of random or partially degenerate, directed phosphopeptide libraries, *see, e.g., Songyang, Z. et al., Cell 72:767-778(1993)*).

Polypeptides of the present invention may also include polypeptides that can be isolated from nature or can be produced by recombinant and/or synthetic means. Such native sequence polypeptides specifically refers to naturally-occurring truncated or secreted forms (*e.g., an extracellular domain sequence*), as well as naturally occurring variant forms (*e.g., alternatively spliced forms*), and naturally occurring allelic variants of the named polypeptides.

The term variant refers to any polypeptide having an amino acid sequence, in comparison to the amino acid sequences of the polypeptides of the present invention, in which one or more amino acids have been substituted with other amino acids; where the substituted amino acids allow or require the polypeptide to assume the equilibrium conformation of the domain of the parent protein. Often, cysteine, lysine and glutamic acid will be used for their side chains which can form covalent linkages to restrict the conformation of a peptide. The term variant refers to any polypeptide in which one or more amino acids are added and/or substituted and/or deleted and/or inserted at the N- or C-terminus or anywhere within the corresponding native sequence, and which retains signal transduction mediation activity of the corresponding native polypeptide. The variants herein preferably comprise a sequence that has at least about 80% sequence identity, more preferably at least about 85% sequence identity, even more preferably at least about 90% sequence identity, most preferably at least about 95% sequence identity, with the amino acid sequence of SEQ ID NOS: 1, 4, 6, 7, 8 or 9.

In such amino acid sequences, one or more amino acids in the fundamental sequence may preferably be substituted with another amino acid(s), the charge and polarity of which is similar to that of the native amino acid, *i.e.*, a conservative amino acid substitution, resulting in a silent change. Substitutes for an amino acid within the fundamental polypeptide sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids; (2) basic amino acids; (3) neutral polar amino acids; and (4) neutral non-polar amino acids. Representative amino acids within these various groups include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cyteine, cystine, tyrosine, asparagine, and glutamine; (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

The term variant shall also include any polypeptide having one or more amino acids deleted from or added to an amino acid sequence of a mediator of signal transduction, but which still retains signal transduction mediation activity. The term fragment shall refer to any shorter version of the polypeptides herein, wherein the fragment is capable of mediating signal transduction.

Sequence identity is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in a native polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. The % sequence identity values are preferably generated by the NCBI BLAST2.0 software as defined by Altschul et al., (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.*, 25:3389-3402. The parameters are set to default values, with the exception of the Penalty for mismatch, which is set to -1. Other algorithms, such as GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package (Genetics Computer Groups, 575 Science Dr., Madison, WI), are also suitable. The selection of the non-default parameters to achieve maximum sequence identity is well within the skill of a person skilled in the art.

Antibodies of the present invention may include any polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab')₂ and FAb fragments, and epitope-binding fragments thereof.

Without further elaboration, one skilled in the art with the preceding description can utilize the present invention to its fullest extent. The following examples are illustrative only, and not intended to limit the remainder of the disclosure in any way.

Example 1 Isolation and characterization of 19G5 clones from rat, mouse and human

Isolation of partial and full-length 19G5 clones from rat, mouse and human

Microarray technology was used to identify genes that are differentially expressed in normal and diseased rat heart. A sequence designated as 19G5 was down regulated in 12-week myocardial infarct (MI) rat hearts. A rat cDNA clone corresponding to 19G5 (R19G5) was isolated and nucleotide sequence determined. The deduced amino acid sequence of the clone revealed homology to the catalytic domain of kinases, thus suggesting that the protein product of R19G5 might be involved in signal transduction. A hybridization of multiple tissue Northern blot with the R19G5 probe showed that the gene is highly expressed in heart as a 2 kb and 4.4 kb transcripts (Figure 8).

A full length cDNA for the 2 kb R19G5 transcript was cloned using 5' RACE technique. The R19G5 has an open reading frame of 1644 base pairs which encodes a protein of 548 amino acids (SEQ ID NO: 8)

A mouse 19G5 (M19G5) EST clone was identified by searching the EST database. Northern blot hybridization using the M19G5 EST clone as probe detected a major transcript of 2 kb in heart. There is also a low level of expression in lung. The smeary hybridization was also detected as in the rat and human but was less prominent. M19G5 was also expressed in 17-day old mouse embryos suggesting that it may play a role in embryo development. Sequence analysis of the M19G5 clone showed that it is 1900 base pairs long and has an open reading frame of 1644 base pairs coding for a polypeptide of 548 amino acids (SEQ ID NO: 9), suggesting that it likely represents full length 2 kb transcript.

A number of human cDNA clones corresponding to 19G5 (H19G5) were isolated from human cDNA library using R19G5 as a probe. Figure 1 shows eight overlapping cDNA clones of H19G5. Extensive overlap among these clones helped build a consensus nucleotide sequence (SEQ ID NO: 2) designated as H19G5 contig. The sequence corresponds to a major transcript (~5 kb) expressed in human heart. The sequence of the contig revealed that it is complete at the 3'-end since it contains a polyadenylation signal (AATAAA) as well as polyA residues at the 3'-end. It has a potential open reading frame, coding for 1351 amino acid residues, that extends beyond the 5'-end of the contig indicating that it is incomplete at the 5'-end. The deduced amino acid sequence (SEQ ID NO: 1) revealed a protein kinase domain at the C-terminal end (amino acid residues 1056 to 1309) and also a partial protein kinase domain towards the N-terminal end (amino acid residues 1 to 105) of this truncated clone. The sequence information of this contig (SEQ ID NO: 2) was used to devise antisense primers corresponding to the 5'-end, which were used in 5' RACE (rapid amplification of cDNA ends) to isolate cDNA clones with longer inserts. A cDNA clone containing full-length coding sequence was isolated. The nucleotide sequence of the clone (SEQ ID NO: 3) revealed an open reading frame that could potentially code for 1667 amino acids long full-length polypeptide (SEQ ID NO: 4).

Using the 5' RACE technique, the full coding region for one of the larger H19G5 (3 kb or 5 kb) transcripts was cloned. It has an open reading frame of 2613 base pairs encoding a protein of 811 amino acids.

Figure 2 shows the amino acid sequence alignment of the three full-length 19G5 proteins. Both the R19G5 (SEQ ID NO: 8) and M19G5 (SEQ ID NO: 9) proteins overlap with the C-terminal two-third of a splicing variant of the H19G5 protein (SEQ ID NO: 7). The identity between the R19G5 and M19G5 proteins is 97%. The three proteins are 85% identical in their sequences.

In order to understand the genomic organization of H19G5 gene, phage genomic library was screened and eleven H19G5 genomic clones were isolated. Restriction enzyme mapping of these clones detected no polymorphism, suggesting that H19G5 may be a single copy gene. The entire genomic DNA region encompassing H19G5 was sequenced and found to contain at least 10 exons and 9 introns as shown in Figure 3.

5 One of the H19G5 cDNA clones contained deletion of two amino acid residues (alanine and proline) in the kinase domain. Sequence analysis of the genomic H19G5 DNA revealed an intron located immediately upstream of the alanine residue. There are two adjacent splicing acceptor sites that are four nucleotides apart at the 3' end of the intron. A splicing event using the first acceptor site generates a protein that includes the two residues, alanine and proline. Utilization of the second splicing acceptor site creates a H19G5 protein with the two amino acids deleted in
10 its kinase domain. These two residues are highly conserved among all kinases. This deletion form of H19G5 protein may thus exhibit reduced or no kinase activity at all, and may serve as a dominant negative inhibitor of the kinase activity of H19G5. This provides a possible mechanism to regulate the activity of H19G5 *in vivo*.

Isolation of cDNA clones of splicing variants of H19G5

15 Multiple transcripts were detected in Northern analysis of human and rat cells, particularly in heart tissues (As shown in Figs. 8 and 9). However, the restriction analysis of the genomic clones and Southern analysis of genomic DNA suggested single-copy nature of H19G5 gene. These observations indicated the possibility of alternative splicing as a source of multiple transcripts. Four cDNA clones representing various splicing variants were isolated and are schematically shown in Figure 4. Complete nucleotide sequence (SEQ ID NO: 5) of the longest clone C11 was
20 determined and the amino acid sequence of a large open reading frame contained therein was deduced (SEQ ID NO: 6). The large ORF has a potential to encode a protein of 2596 amino acid residues. The sequence analysis revealed the presence of a number of structurally and functionally important domains in H19G5. The presence of some of the domains strengthens the possibility of the involvement of H19G5 in signal transduction. For example, H19G5 has two kinase domains, one at the N-terminal (1094 to 1351 amino acid residues, N-KD) and the other at the C-terminal
25 (2301 to 2553 amino acid residues, C-KD) end. H19G5 also has a Guanine nucleotide Exchange Factor (GEF) domain (325 to 504 amino acid residues), and a Pleckstrin Homology (PH) domain (532 to 634 amino acid residues). Additionally, H19G5 contains five Immunoglobulin (Ig) like domains distributed throughout the sequence.

Structural and functional features of full-length H19G5 protein sequence

30 The full-length H19G5 amino acid sequence (SEQ ID NO: 6) shows sequence similarity to some functionally important domains of a protein called Trio. The comparison of the domain structure of H19G5 and Trio is schematically depicted in Figure 5. Both kinase domains of H19G5 (N-KD and C-KD) are homologous to a single kinase domain of Trio as well as to a kinase domain of smooth muscle-myosin light chain kinase (SM MLCK) as shown in Figure 6. The identity between H19G5 N-KD and Trio KD is about 40% and between H19G5 N-KD and SM MLCK is

about 38%. The sequence identity between the two kinase domains of H19G5 is about 30%. A single GEF domain of H19G5 is homologous to both GEF domains (GEF-D1 and GEF-D2) of Trio as shown in Figure 7.

Proteins containing GEF domains are involved in signal transduction (for a review, see Cherfils and Chardin, *Trends Biochem. Sci.* 24: 306-311 [1999]). GEF domains promote exchange of GTP for GDP on GTP-binding proteins (G proteins) and thereby positively regulate their activities. As these proteins harbor intrinsic GTPase activity, they are also referred to as GTPases. These small G proteins, as opposed to trimeric G proteins, belong to a superfamily of Ras-like proteins. These proteins are bound to the inner face of plasma membrane, and usually exist in GDP-bound "inactive" state. When a ligand interacts with a membrane bound receptor, alteration of conformation allows the receptor to interact with a G protein. This interaction results in conformational change in the G protein that weakens the affinity for GDP and leads to replacement of GDP with GTP. This nucleotide exchange is greatly accelerated or promoted by proteins containing GEF domains. Once bound to GTP, the G proteins assume an "active" state in which they interact with the downstream effectors and facilitate transduction of signal from membrane to the nucleus. However, the activity of the G proteins is tightly controlled as their intrinsic GTPase activity rapidly hydrolyzes bound GTP into GDP and restores "inactive" status. Thus, G proteins function as molecular switches in signal transduction. A number of membrane receptors operate through G proteins. The downstream effectors of the activated G proteins include various protein kinases constituting a cascade of protein phosphorylation that brings about a desired change in gene expression.

As discussed in the preceding section, GEF domains play a critical role in signal transduction by controlling the activation of G proteins. Trio is a complex protein possessing two GEF domains, each with adjacent pleckstrin homology (PH) domains and Src Homology-3 (SH3) domains, a protein serine/threonine kinase domain with an adjacent immunoglobulin-like domain and multiple spectrin-like domains (Medley *et al.*, *J. Cell Sci.* 112: 1825-1834 [1999]). Trio cDNA clone was isolated by virtue of its ability to interact with protein tyrosine phosphatase (PTP) domain of a protein called LAR (Debant *et al.*, *Proc. Natl. Acad. Sci. USA* 93: 5466-5471 [1996]). LAR is a broadly expressed transmembrane protein tyrosine phosphatase comprised of a cell adhesion-like extracellular region and two intracellular PTPase domains, and is proposed to regulate cell-matrix interactions (Mourey and Dixon, *Curr. Opin. Gen. Dev.* 4: 31-39 [1994]). Trio represents a unique member of the Rho-GEFs family possessing two functional GEF domains of distinct specificities. For example, GEF1 is specifically active on Rac1 GTPase, while GEF2 targets RhoA GTPase (Debant *et al.*, *supra*). This unique feature allows Trio to link Rho and Rac specific signalling pathways *in vivo*.

The Rho family of Ras-like GTPases includes Rac (1, 2 and 3), RhoG, Cdc42Hs, TC10, TTF/RhoH, Rho (A, B and C), RhoD, RhoE, and RhoL. These proteins and other Ras-like proteins constitute Ras superfamily of structurally and functionally related GTPase proteins. These proteins are involved in diverse physiological functions such as control of cell shape (reviewed in Tapon and Hall, *Curr. Opin. Cell Biol.* 9: 86-92 [1997]), cell motility (Aepfelbacher *et al.*, *Proc. Natl. Acad. Sci. USA* 91: 4263-4267 [1994]; and *Curr. Biol.* 6: 70-75 [1996]), cell polarity (Adams *et al.*, *J. Cell Biol.* 111: 131-142 [1990]), smooth muscle contraction (Hirata *et al.*, *J. Biol. Chem.* 267: 8719-8722 [1992]), cell

adhesion (Nobes and Hall, *Cell* 81: 53-62 [1995]; Braga *et al.*, *J. Cell Biol.* 137: 1421-1431 [1997]), cell division (Dutartre *et al.*, *J. Cell Sci.* 109:367-377 [1996]), vesicular transport between organelles such as receptor-mediated endocytosis (Lamaze *et al.*, *Nature* 382: 177-179 [1996]), apoptosis (Esteve *et al.*, *Oncogene* 11: 2657-2665 [1995]; Jimenez *et al.*, *Oncogene* 10: 811-816 [1995]; Gulbins *et al.*, *J. Biol. Chem.* 271: 26389-26394 [1996]; Moorman *et al.*, *J. Immunol.* 156: 4146-4153 [1996]; Brenner *et al.*, *J. Biol. Chem.* 272: 22173-22181 [1997]) and normal and pathological cell proliferation (Olson *et al.*, *Science* 269: 1270-1272 [1995]; Hirai *et al.*, *J. Biol. Chem.* 272: 13-16 [1997]; Khosravi-Far *et al.*, *Mol. Cell. Biol.* 16: 3923-3933 [1996]; Qiu *et al.*, *Mol. Cell. Biol.* 17: 3449-3458 [1997]; Roux *et al.*, *Curr. Biol.* 7: 629-637 [1997]).

The presence of a GEF domain and protein kinase domains along with its homology to Trio suggests that H19G5 may possess guanine nucleotide exchange factor activity and protein kinase activity, both of which are shared by a number of proteins involved in signal transduction.

Expression pattern of 19G5 in rat and human tissues

Northern blot analysis revealed that R19G5 gene is highly expressed in heart as a 2 kb and a 4.4 kb transcripts (Figure 8). Hybridization was performed using multiple tissue Northern blot (Clontech, Palo Alto, CA) and ExpressHyb solution following the manufacturer's protocol. The R19G5 probe also hybridized to mRNAs from skeletal muscle and detected multiple weak bands. High background observed in a lane corresponding to skeletal muscles is not due to RNA degradation as probing of the same blot with β -actin probe detected the right sized transcripts with a clean background (Figure 8). The significance of the high background in skeletal muscle is not clear. Expression of R19G5 was not detected in brain, kidney, spleen, lung, liver, and testis.

Hybridization of human multiple tissue Northern blot (Clontech, Palo Alto, CA) with H19G5 probe detected a strong transcript of about 5 kb and three minor transcripts of about 3 kb, 2.4 kb, and 1.8 kb in heart tissue (Figure 9). There were multiple transcripts and high background in skeletal muscle as seen with rat tissue. Only the 3 kb transcript was detected in human fetal heart. There is a low level expression of the 2.4 kb transcript in brain. H19G5 expression was not detected in spleen, lung, liver, kidney, pancreas, thymus, prostates, testis, ovary, small intestine, colon, peripheral blood leukocyte, stomach, thyroid, spinal cord, lymph node, trachea, adrenal gland, bone marrow, uterus muscle, or bladder muscle by Northern blot.

In order to determine whether the multiple transcripts of 19G5 in human heart are derived from alternative splicing or multiple gene copies, Southern blot analysis of genomic DNA was performed with H19G5 probe (Figure 10). The results suggest that H19G5 is a single copy gene. This is consistent with the lack of detection of polymorphism in the restriction analysis of the genomic clones of H19G5.

Functional characterization of H19G5 protein

A 20 amino acid peptide from the C-terminus of H19G5 protein (SEQ ID NO: 1) was used to raise polyclonal antibodies in rabbits. Affinity purified rabbit anti-H19G5 antiserum has been obtained. Two different GST-H19G5 fusion proteins were used as antigens to generate mouse monoclonal anti-H19G5 antibodies. One of the antigens used was a GST-H19G5 fusion protein containing amino acid residues 610 to 811 of SEQ ID NO: 1. Many clones of anti-H19G5 monoclonal antibodies were obtained. Three of them were shown to recognize recombinant H19G5 proteins expressed in mammalian cells by Western analysis and immunocytochemistry. The antibodies may be used to determine the size and localization of 19G5 protein by Western blot and immunohistochemistry.

Subcellular localization of H19G5 protein was determined using confocal microscopy on cells transfected with vectors expressing 19G5 proteins fused to Green Fluorescent Protein (GFP). Three 19G5-GFP fusion protein expression constructs were made using three different 19G5 cDNA clones, the longest human 19G5 clone C11 [H19G5(C11)-GFP], a 2.7 kb clone of human 19G5 containing the C-terminal kinase domain [H19G59F1)-GFP], and the rat 19G5 small transcript [R19G5(S)-GFP]. The control GFP vector and the 19G5-GFP fusion expression constructs were transfected into C2C12 cells (ATCC Catalog No. CRL-1772). Cells were grown on chamber slides and transfected using SuperFectamine reagent from Qiagen for 3 hrs. Cells were fixed 24 hrs post-transfection with 4% paraformaldehyde for 15 min at room temperature and examined using a confocal microscope. The two longer forms of human 19G5-GFP proteins were detected in the nuclei whereas the short rat 19G5-GFP fusion protein was detected in the cytoplasm (Figure 11). This suggests that different forms of 19G5 proteins are localized in different regions in the cells and may have different functions. Since the gene is normally expressed in heart, the localization of 19G5 protein in cardiac myocytes may be examined. Antisense constructs to study the effects of inhibiting the activity of 19G5 protein on cardiac myocytes may also be made and used.

A possibility that H19G5 might interact with various G proteins, as suggested by the presence of GEF domain and homology with Trio, was examined. HEK 293 cells constitutively expressing Epstein-Barr Virus Nuclear Antigen (EBNA) (Invitrogen, San Diego, CA) were transfected with H19G5-C11 expression construct. The eukaryotic vector used for 19G5 expression, pEAK8 (EdgeBiosystems), contains Epstein-Barr virus (EBV) origin of DNA replication, which allows replication of the expression construct in transfected cells thereby amplifying the level of protein expression. After 24 hrs, one 10 cm dish of transfected 293 EBNA cells were lysed with 1 ml of lysis buffer (1X PBS, 0.1% Triton, and proteinase inhibitors (0.2 mM AEBSF, 0.16 μ M Aprotinin, 0.01 mM Bestatin, 3 μ M E-64, 4 μ M Leupeptin, and 2 μ M Pepstatin) on ice for 30'. Cells were then homogenized with a dounce homogenizer on ice. The lysates were cleared by centrifugation. One ml of the cleared lysate was incubated with 5 μ g of various small G proteins, expressed as GST fusion proteins and bound to glutathione-agarose beads, at 4° C for 2 hrs. The protein-agarose complex was pelleted by brief centrifugation and washed for 4 times 5' each with the lysis buffer at room temperature. The complex was then resuspended in SDS sample buffer, boiled and run on a SDS-PAGE and Western blotted with an anti-H19G5 monoclonal antibody. As shown in Figure 12, H19G5 was found to bind to Cdc42. No binding was detected with Rac1 or RhoA. Lane 8 is His-tagged Cdc42 and in lane 9 His-tagged Cdc42-agarose

complex was boiled for 5' before adding to the H19G5 cell lysate. This result showed that H19G5 specifically interacts with Cdc42 protein and there is no non-specific interaction with agarose beads. The results presented herein suggest that 19G5 protein may play an important role, by virtue of regulating a small GTPase such as Cdc42Hs, in a variety of cellular activities. For example, Cdc42 has been shown to regulate actin polymerization and focal adhesion complex formation which in turn is necessary for filopodia formation (Nobes and Hall, *Cell* 81: 53-62 [1995]). Cdc42 and rac have also been shown to regulate Jun N-terminal kinase (JNK) activity via the MAP kinase pathway (Coso *et al.*, *Cell* 81: 1137-1146 [1995]; Minden *et al.*, *Cell* 81: 1147-1157 [1995]; Olson *et al.*, *Science* 269: 1270-1272 [1995]), an evolutionarily conserved and ubiquitous signal transduction pathway that impacts upon a number of important cellular functions.

10 C2C12 myoblasts cells (ATCC Catalog No. CRL-1772) can be induced to differentiate into myotubes when placed in a medium containing 2% horse serum (Lechner *et al.*, *Proc. Natl. Acad. Sci. USA* 93: 4355-4359 [1996]). Figure 13 shows phase contrast micrographs of C2C12 myoblasts undergoing differentiation into myotubes. At Day 0, undifferentiated C2C12 cells with typical myoblast morphology can be seen. Once induced to differentiate, as shown here at Day 3 and 5 after induction, an increasingly larger number of cells with typical morphology of differentiated myotubes, i.e. large, elongated, multinucleated syncytial cells, could be seen. The induction of Myogenin expression was monitored during differentiation. Myogenin is not expressed in myoblasts, however, its expression is strongly induced when myoblasts undergo differentiation into myotubes. Thus, it acts as a biochemical marker of myotubes. Figure 14 shows induction of myogenin protein expression when C2C12 myoblast cells are induced to differentiate into myotubes. C2C12 cells were cultured and induced to differentiate by placing in a medium containing 20 2% horse serum. Cells were lysed in radioimmunoprecipitation (RIPA) buffer (1X PBS containing 1% Igepal CA-630, 0.5% sodium deoxycholate and 0.1% SDS) on ice for 30'. Total lysates were cleared by centrifugation at 10,000 rpm for 10'. Protein concentration of each lysate was measure using the BCA method. SDS sample buffer was added to the total lysate and boiled for 3'. Equal amount of total protein of each sample was run on SDS-PAGE and blotted using an anti-myogenin monoclonal antibody. The result demonstrated that Myogenin expression was induced 25 concomitantly with differentiation of C2C12 myoblasts into myotubes under the conditions used for induction.

The expression of 19G5 RNA was also monitored at various stages during differentiation of myoblasts into myotubes. Undifferentiated C2C12 cells were plated on 6 cm dishes at 2.4×10^4 cells/cm² and cultured in growth medium with 10% fetal bovine serum for 24 hrs to about confluence. Cells were washed with PBS and induced to differentiate into myotubes in differentiation medium with 2% horse serum. Total RNA was isolated from cells at 1, 30 2, or 4 days post-induction using Qiagen's Rneasy kit according to the manufacture's instruction. The expression of 19G5 transcript was analyzed using Taqman assay. One microgram of total RNA, isolated at various time points post-induction, was reverse transcribed into cDNA using PE Biosystems Reagents and Multiscribe enzyme according to manufacture's instruction. Ten ng of cDNA was added to 1X master mix, and the primers and probe for the gene of interest were added according to manufacture's instructions. The reaction were carried out in the ABI Prism 7700

Detection System. The quantity of 19G5 and the quantity for 18S were determined for each sample, and the ratio of 19G5/ 18S was used to evaluate differences in the level of 19G5 expression in various samples. Comparison of the values thus obtained with pre-induction values allowed to determine fold induction of 19G5 expression during differentiation. As shown in Figure 15, expression of 19G5 transcript was significantly increased during differentiation of C2C12 myoblasts into myotubes. The level of induction reached to about 10-fold at 4 days post-induction. Increased expression of 19G5 likely reflects a specific function in myotubes.

TGF- β is known to inhibit differentiation of C2C12 myoblast into myotubes (Katagiri *et al.*, *J. Cell Biol.* 127: 1755-1766 [1994]; Namiki *et al.*, *J. Biol. Chem.* 272: 22046-22052 [1997]). Therefore, the effect of TGF- β on the induction of expression of 19G5 during differentiation of C2C12 cells was examined. C2C12 cells were plated in 6 cm dishes at 2.4×10^4 cells/cm² and cultured in the growth medium for 24 hours. Cells were then rinsed with PBS and induced to differentiate for 4 days in the medium containing 5% fetal bovine serum either in the absence or in the presence of 10 ng/ml of TGF- β . Total RNA was isolated from cells using Qiagen's Rneasy kit. Induction of 19G5 expression in TGF- β treated or untreated cells over undifferentiated C2C12 cells was measured by Taqman assay. As shown in Figure 16, the induction of 19G5 expression during C2C12 differentiation is inhibited by TGF- β . TGF- β is a powerful regulator of cell growth and differentiation and regulation of expression of 19G5 by TGF- β likely represents an important physiological event with significant relevance to normal and abnormal changes in cardiac cells. Furthermore, the results suggest a possible involvement of 19G5 in myogenesis.

Example 2 (Polypeptides which can mediate signal transduction)

The polypeptides of the present invention, such as the specific embodiment shown in SEQ ID NOs: 1, 4, 6, 7, 8 or 9 may be prepared by any known techniques. Conveniently, the polypeptides may be prepared using the solid-phase synthetic technique initially described by Merrifield in *J. Am. Chem. Soc.* 15:2149-2154 (1963). Other peptide synthesis techniques may be found, for example, in M. Bodanszky *et al.*, PEPTIDE SYNTHESIS, John Wiley & Sons, 2d Ed. (1976) as well as in other reference works known to those skilled in the art. A summary of peptide synthesis techniques may be found in J. Stuart and J.D. Young, SOLID PHASE PEPTIDE SYNTHESIS, Pierce Chemical Co., Rockford, IL (1984). The synthesis of peptides by solution methods may also be used, as described in THE PROTEINS, Vol-II, 3d Ed., Neurath, H. *et al.*, Eds., p.105-237, Academic Press, New York, NY (1976). Appropriate protective groups for use in such syntheses will be found in the above texts as well as in J.F.W. McOmie, PROTECTIVE GROUPS IN ORGANIC CHEMISTRY, Plenum Press, New York, NY (1973). In general, these synthetic methods involve the sequential addition of one or more amino acid residues or suitably protected amino acid residues to a growing peptide chain. Normally, either the amino or carboxyl group of the first amino acid residue is protected by a suitable, selectively-removable protecting group. A different, selectively-removable protecting group is utilized for amino acids containing a reactive side group, such as lysine.

Using a solid phase synthesis as an example, the protected or derivatized amino acid is attached to an inert solid support through its unprotected carboxyl or amino group. The protecting group of the amino or carboxyl group is then selectively removed and the next amino acid in the sequence having the complementary (amino or carboxyl) group suitably protected is admixed and reacted under conditions suitable for forming the amide linkage with the residue already attached to the solid support. The protecting group of the amino or carboxyl group is then removed from this newly added amino acid residue, and the next amino acid (suitably protected) is then added, and so forth. After all the desired amino acids have been linked in the proper sequence, any remaining terminal and side group protecting groups (and solid support) are removed sequentially or concurrently, to provide the final peptide. The polypeptides of the invention preferably are devoid of benzylated or methylbenzylated amino acids. Such protecting group moieties may be used in the course of synthesis, but they are removed before the polypeptides are used. Additional reactions may be necessary, as described elsewhere to form intramolecular linkages to restrain conformation, if desired. The polypeptides of the present invention may also be linked to an additional sequence of amino acids either or both at the N-terminus and at the C-terminus. Such additional amino acid sequences, or linker sequences, can be conveniently affixed to a detectable label, solid matrix, or carrier. Typical amino acid residues used for linking are tyrosine, cysteine, lysine, glutamic acid and aspartic acid, or the like.

Of course, the present polypeptides may also be prepared by recombinant DNA techniques as described, for example, in Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, Chapters 1-18, Second Edition (Cold Spring Harbor NY 1989), and as detailed in Examples 3-4 *infra*. The present invention also relates to vectors comprising DNA molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Host cells may be genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are preferably those previously used with the host cell selected for expression, and will be apparent to the skilled artisan.

Example 3 (Hosts, Vectors and DNA encoding polypeptides which can mediate signal transduction)

The DNA molecules of the present invention may be employed for producing the polypeptides of the present invention by recombinant techniques. More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences broadly described above. Thus, for example, the DNA molecule sequence may be included in any one of a variety of expression vehicles, in particular vectors or plasmids for expressing such a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, *e.g.*, derivatives of SV40; bacterial plasmids; phage DNA; yeast plasmids; vectors derived from combinations of plasmids and phage DNA;

viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. The following vectors are provided by way of example. Bacterial: pQE7D, pQE6D, pQE-9 (Qiagen), pBS, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTRC99A, pKK223-3, pKK233-3, pDR540, PRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene); pSVK3, pBPV, pMSG, PSVL (Pharmacia). However, any other
5 vector or plasmid may be used as long as they are replicable and viable in the host. The vector containing the appropriate DNA sequence, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the polypeptides of the present invention. Representative examples of appropriate hosts include: bacterial cells, such as *E. coli*, *Salmonella typhimurium*, *Streptomyces*; fungal cells, such as yeast; insect cells, such as *Drosophila* S2 and *Spodoptera* Sf9; animal cells, such as CHO, COS or Bowes melanoma;
10 adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

15 The DNA sequence in the expression vector may be operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Suitable promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, λ P_R, P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus,
20 and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of skill in the art. The expression vector may also contain a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably may contain a gene to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such
25 as tetracycline or ampicillin resistance in *E. coli*.

An embodiment of the invention is an isolated DNA molecule comprising the nucleotide sequence of SEQ ID NOS: 2, 3 or 5. This nucleotide sequence, or fragments or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of the polypeptides of the present invention, or functionally active peptides or functional equivalents thereof, in appropriate host cells. Due to the degeneracy of the nucleotide
30 coding sequence, other DNA sequences which encode substantially the same amino acid sequences as depicted in SEQ ID NOS: 1, 4, 6, 7, 8 or 9, or analogs or fragments thereof, may be used in the practice of the invention for the cloning and expression of a mediator of signal transduction. Such alterations include deletions, additions or substitutions of different nucleotide residues resulting in a sequence that encodes the same or a functionally equivalent gene product. The gene product may contain deletions, additions or substitutions of amino acid residues within the sequence, which

result in a silent change thus producing a bioactive product. Such amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, the amphipathic nature of the residues involved and/or on the basis of crystallographic data. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; amino acids with uncharged polar head groups having similar hydrophilicity values include the following: leucine, isoleucine, valine; glycine, alanine; asparagine, glutamine; serine, threonine; phenylalanine, tyrosine.

Techniques well known to those skilled in the art for the isolation of DNA, generation of appropriate restriction fragments, construction of clones and libraries, and screening recombinants may be used. For a review of such techniques, see, for example, Sambrook, *et al.*, *supra*, the disclosure of which is hereby incorporated by reference. Also, the 5' untranslated and coding regions of the nucleotide sequence could be altered to improve the translational efficiency of the mRNA. In addition, based on X-ray crystallographic data, sequence alterations could be undertaken to improve protein stability, *e.g.*, introducing disulfide bridges at the appropriate positions, and/or deleting or replacing amino acids that are predicted to cause protein instability. These are only examples of modifications that can be engineered to produce a more active or stable protein, more protein, or even change the substrate specificity of the protein.

Example 4 (Cells transformed with recombinant vectors containing DNA encoding polypeptides which can mediate signal transduction)

In a further embodiment, the present invention relates to host cells containing the above-described construct. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. The host cell preferably may secrete the recombinant protein. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (L. Davis *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY, 1986)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, *supra*.

Transcription of a DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually from about 10 to 300 bp, that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the

late side of the replication origin (base pair 100 to 270), a cytomegalovirus early promoter enhancer, a polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is preferably assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use may be constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation, initiation and termination signals in operable reading phase with a functional promoter. The vector may comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI). These pBR322 backbone sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be de-repressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells may be cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Various mammalian cell culture systems can also be employed to express recombinant polypeptides. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell*, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors may comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation sites, splice donor and acceptor sites, transcriptional termination sequences,

and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

5 The polypeptides of the present invention may be recovered and purified from recombinant cell cultures by methods used heretofore, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

10 The polypeptides of the present invention may be a naturally purified product, or a product of chemical synthetic-procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated. Polypeptides of the invention may also include an initial
15 methionine amino acid residue.

In particular, two baculovirus expression constructs of a wild-type and a mutant H19G5 C-terminal kinase domain have been constructed. The wild-type kinase domain construct was made by cloning a cDNA fragment which encodes the amino acid residues 1002 to 1314 of the H19G5 contig protein sequence into the pFastBac HTc vector. The mutant kinase domain construct contains the same amino acid sequence as the wild-type kinase domain except
20 that Tyr residue at position 1213 was changed to a Glu in an attempt to create a constitutively active kinase. Both recombinant proteins contain a his-tag at the N-terminus.

Example 5 (Pharmaceutically acceptable salts of polypeptides which can mediate signal transduction)

Any peptide of the present invention may be used in the form of a pharmaceutically acceptable salt.
25 Suitable acids which are capable of forming salts with the peptides of the present invention include inorganic acids such as hydrochloric acid, hydrobromic acid, perchloric acid, nitric acid, thiocyanic acid, sulfuric acid, phosphoric acid and the like; and organic acids such as formic acid, acetic acid, propionic acid, glycolic acid, lactic acid, pyruvic acid, oxalic acid, malonic acid, succinic acid, maleic acid, fumaric acid, anthranilic acid, cinnamic acid, naphthalene sulfonic acid, sulfanilic acid, and the like.

30 Suitable bases capable of forming salts with the peptides of the present invention include inorganic bases such as sodium hydroxide, ammonium hydroxide, potassium hydroxide and the like; and organic bases such as mono-, di- and tri-alkyl and aryl amines (*e.g.*, triethylamine, diisopropyl amine, methyl amine, dimethyl amine and the like) and optionally substituted ethanolamines (*e.g.*, ethanolamine, diethanolamine and the like).

Example 6 (Pharmaceutical compositions containing polypeptides which can mediate signal transduction)

For use in a method of identification, prevention or treatment, such as the identification, prevention or treatment of infection of a mammalian host by a microorganism, the polypeptides of the present invention may be present in a pharmaceutical composition in admixture with a pharmaceutically acceptable sterile vehicle. The pharmaceutical composition may be compounded according to conventional pharmaceutical formulation techniques.

The vehicle may take a wide variety of forms depending on the form of preparation desired for administration, *e.g.*, sublingual, rectal, nasal, oral or parenteral. Compositions for oral dosage form may include any of the usual pharmaceutical media, such as, for example, water, oils, alcohols, flavoring agents, preservatives, coloring agents and the like in the case of oral liquid preparations (*e.g.*, suspensions, elixirs and solutions) or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (*e.g.*, powders, capsules and tablets). Controlled release forms may also be used. Because of their ease in administration, tablets and capsules represent an advantageous oral dosage unit form, in which case solid pharmaceutical carriers may be employed. If desired, tablets may be sugar coated or enteric coated by standard techniques.

For compositions to be administered parenterally, the carrier will usually comprise sterile water, although other ingredients to aid solubility or for preservation purposes may be included. Injectable suspensions may also be prepared, in which case appropriate liquid carriers, suspending agents and the like may be employed. The parenteral routes of administration may be intravenous injection, intramuscular injection or subcutaneous injection.

For intravenous administration, the polypeptides may be dissolved in an appropriate intravenous delivery vehicle containing physiologically compatible substances such as sodium chloride, glycine and the like, having a buffered pH compatible with physiologic conditions. Such intravenous delivery vehicles are known to those skilled in the art.

The polypeptides of the invention may be administered to subjects where mediation of signal transduction is desired. The peptides may be administered by any convenient means that will result in the delivery to the subject of an effective amount to mediate signal transduction. Oral administration is presently contemplated as a preferred administration route. The amount administered will depend on the activity of the particular compound administered, which may readily be determined by those of ordinary skill in the art.

Example 7 (Monoclonal antibodies against polypeptides which can mediate signal transduction)

Another embodiment of the present invention relates to a monoclonal antibody to the polypeptides of the present invention (or an antigenic portion thereof), which may be produced by methods recognized in the art, including the formation of monoclonal antibody-producing hybridomas (Kohler, G., and C. Milstein, *Nature* 256:495-497 (1975); *Eur. J. Immunol.* 6:511-519 (1976)). By fusing antibody-forming cells (spleen lymphocytes) with myeloma cells (malignant cells of bone marrow primary tumors), a hybrid cell line is created from a single fused cell hybrid (called a

hybridoma or clone) having certain inherited characteristics of both the lymphocytes and myeloma cell lines. Like the lymphocytes (taken from animals primed with sheep red blood cells as antigen), the hybridomas secreted a single type of immunoglobulin specific to the antigen; moreover, like the myeloma cells, the hybrid cells had the potential for indefinite cell division. The combination of these two features offered distinct advantages over conventional antisera.

5 Whereas antisera derived from vaccinated animals are variable mixtures of polyclonal antibodies which never can be reproduced identically, monoclonal antibodies are highly specific immunoglobulins of a single type. The single type of immunoglobulin secreted by a hybridoma is specific to one and only one antigenic determinant, or epitope, on the antigen, a complex molecule having a multiplicity of antigenic determinants. For instance, if the antigen is a protein, an antigenic determinant may be one of the many peptide sequences (generally 6-7 amino acids in length (Atassi, M.Z.,
10 *Molec. Cell. Biochem.* 32:21-43 (1980)) within the entire protein molecule. Hence, monoclonal antibodies raised against a single antigen may be distinct from each other depending on the determinant that induced their formation; but for any given clone, all of the antibodies it produces are identical. Furthermore, the hybridoma cell line can be reproduced indefinitely, is easily propagated *in vitro* or *in vivo*, and yields monoclonal antibodies in extremely high concentration.

15

Example 8 (Therapeutic monoclonal antibodies against polypeptides which can mediate signal transduction)

The monoclonal antibodies of the present invention can have potential immunotherapeutic value (Oldham, R.K., *J. Clin. Oncol.*, 1:582-590 (1983); Miller, R.A. *et al.*, *Blood*, 62:988-995 (1983); Miller R.A. *et al.*, *New Engl. J. Med.* 306:517-522 (1982); Ritz, J. and Schlossman, S., *Blood*, 59:1-11 (1982); and Kirch, M.E. and Ulrich, H., *J.*
20 *Immunol.* 127:805-810 (1981) (investigating the therapeutic efficacy in both animal and human subjects)). In addition, the monoclonal antibodies can be used in cytotoxic drug-antibody conjugates similar to those described in Beverly, P.C.L., *Nature*, 297:358-9 (1982); Krolick, K.A. *et al.*, *Nature*, 295:604-5 (1982); Krolick, K.A. *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 77:5419-23 (1980); Arnon, R. and Sela, M., *Immunol. Rev.*, 62:5-27 (1982); Raso, V. *et al.*, *Cancer Res.*, 42:457-64 (1982); and DeWeger, R.A. and Dullens, H.F.J., *Immunol. Rev.* 62:29-45 (1982).

25

In an embodiment of the invention, purified polypeptides of the present invention (or an antigenic portion thereof) can be used as an antigen or immunogen. In addition, microorganisms expressing H19G5 protein or polypeptide fragments thereof also represent potential antigens or sources of antigen with which to immunize animals to obtain somatic cells for fusion. Somatic cells with the potential for producing antibody and, in particular, B lymphocytes, are suitable for fusion with a B-cell myeloma line. Those antibody-producing cells that are in the dividing
30 plasmablast stage fuse preferentially. Somatic cells may be derived from the lymph nodes, spleens and peripheral blood of primed animals and the lymphatic cells of choice depending to a large extent on their empirical usefulness in the particular fusion system. Once-primed or hyperimmunized animals can be used as a source of antibody-producing lymphocytes. Mouse lymphocytes give a higher percentage of stable fusions with mouse myeloma lines. However, the use of rat, rabbit, and frog cells is also possible. Alternatively, human somatic cells capable of producing antibody,

specifically B lymphocytes, are suitable for fusion with myeloma cell lines. While B lymphocytes from biopsied spleens or lymph nodes of individual may be used, the more easily accessible peripheral blood B lymphocytes are preferred. The lymphocytes may be derived from patients with diagnosed carcinomas.

Specialized myeloma cell lines have been developed from lymphocyte tumors for use in hybridoma-producing fusion procedures (Kohler, G., and C. Milstein, *Eur. J. Immunol.* 6:511-519 (1976); M. Schulman *et al.*, *Nature* 276: 269-270 (1978)). Examples of myeloma cell lines that may be used for the production of fused cell hybrids include X63-Ag8, NSI-Ag4/1, MPCII-45.6TGI.7, C63-Ag8.653, Sp2/O-Ag14, FO, and S194/5XXO.BU.1, all derived from mice; 210.RCY3.Agl.2.3, U-226AR, and GM1500GTGAL2, all derived from rats; and U-226AR and GM1500GTGAL2, derived from humans, (G.J. Hammerling, U. Hammerling, and J.F. Kearney (editors), *Monoclonal Antibodies and T-cell Hybridomas* in: J.L. Turk (editor) RESEARCH MONOGRAPHS IN IMMUNOLOGY, Vol. 3, Elsevier/North Holland Biomedical Press, NY (1981)).

Methods for generating hybrids of antibody-producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 proportion (though the proportion may vary from about 20:1 to about 1:1), respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. It is often preferred that the same species of animal serve as the source of the somatic and myeloma cells used in the fusion procedure. Fusion methods have been described by Kohler and Milstein (*Nature* 256:495-497 (1975) and *Eur. J. Immunol.* 6:511-519 (1976), and by Geffer *et al.* (*Somatic Cell Genet.* 3:231-236 (1977)). The fusion-promotion agents used by those investigators were Sendai virus and polyethylene glycol (PEG), respectively.

Once the desired fused cell hybrids have been selected and cloned into individual antibody-producing cell lines, each cell line may be propagated in either of two standard ways. A sample of the hybridoma can be injected into a histocompatible animal of the type that was used to provide the somatic and myeloma cells for the original fusion. The injected animal develops tumors secreting the specific monoclonal antibody produced by the fused cell hybrid. The body fluids of the animal, such as serum or ascites fluid, can be tapped to provide monoclonal antibodies in high concentration. Alternatively, the individual cell lines may be propagated *in vitro* in laboratory culture vessels; the culture medium, also containing high concentrations of a single specific monoclonal antibody, can be harvested by decantation, filtration or centrifugation.

Example 9 (Diagnostic monoclonal antibodies against polypeptides which can mediate signal transduction)

The monoclonal antibodies of this invention can be used as probes in detecting discrete antigens expressed by tissue or cell samples. The expression or lack of expression of these antigens can provide clinically exploitable information that is not apparent after standard histopathological evaluations. It may thus be possible to correlate the immuno-phenotypes of individual tissue or cell samples with various aspects of signal transduction and responsiveness to certain types of therapies, thereby establishing important classifications of prognosis.

The use of the monoclonal antibodies described herein can be extended to the screening of human biological fluids for the presence of the specific antigenic determinant recognized. *In vitro* immunoserological evaluation of sera withdrawn from patients thereby permits non-invasive diagnosis of disease. By way of illustration, human fluids, such as pleural fluids or lymph, can be taken from a patient and assayed for the specific epitope, either as released antigen or membrane-bound on cells in the sample fluid, using monoclonal antibodies against the polypeptides of the present invention in standard radioimmunoassays or enzyme-linked immunoassays known in the art or competitive binding enzyme-linked immunoassays.

The monoclonal antibodies of this invention are potentially useful for targeting diseased tissue or cells *in vivo*. They can therefore be used in humans for localization and monitoring of the microbial infection. For this application, it is preferable to use purified monoclonal antibodies. Purification of monoclonal antibodies for human administration by ammonium sulfate or sodium sulfate precipitation followed by dialysis against saline and filtration sterilization has been described by Miller *et al.* (in: HYBRIDOMAS IN CANCER DIAGNOSIS AND THERAPY, (1982), p. 134).

Alternatively, immunoaffinity chromatography techniques may be used to purify the monoclonal antibodies. The purified monoclonal antibodies can be labeled with radioactive compounds, for instance, radioactive iodine, and administered to a patient intravenously. After localization of the antibodies at the infection site, they can be detected by emission tomographical and radionuclear scanning techniques, thereby pinpointing the location of the infection. Experimental radioimmunodetection with monoclonal antibodies may occur by external scintigraphy.

Passive monoclonal serotherapy may be a potential use for the monoclonal antibodies of this invention. By way of illustration, purified anti-H19G5 monoclonal antibody is dissolved in an appropriate carrier, *e.g.*, saline, with or without human albumin, at an appropriate dosage and is administered to a patient. The monoclonal antibodies are preferably administered intravenously, *e.g.*, by continuous intravenous infusion over several hours, as in Miller *et al.*, *supra*. Infusions can be administered over a period of weeks during which the anti-microbial effects are monitored.

Example 10 (Anti-idiotypic antibodies to antibodies against polypeptides which can mediate signal transduction)

In an alternate embodiment, the antibodies described herein are used to stimulate the production of corresponding anti-idiotypic antibodies. In brief, anti-idiotypic antibodies, or antiidiotypes are antibodies directed against the antigen combining region or variable region (idiotypic) of another antibody. Based on Jerne's network model of idiotypic relationships (Jerne, *Ann. Immunol.* 125:373 (1974); Jerne *et al.*, *EMBO* 1:234 (1982)), immunization with an antibody molecule expressing a paratope (antigen-combining site) for a given antigen should produce a group of anti-antibodies, some of which share with the antigen a complementary structure to the paratope. Immunization with a subpopulation of antiidiotypic antibodies should in turn produce a subpopulation of antiidiotypic antibodies which bind the initial antigen. Thus, the administration of the monoclonal antibodies of the present

invention may result in a modification of the host's immune response, as the consequence of the formation of anti-idiotypic antibodies which may develop during therapy with the monoclonals.

Example 11 (Monoclonal antibody-drug conjugates)

5 The monoclonal antibodies of this invention can be used in conjunction with a broad spectrum of pharmaceutical or cytotoxic agents that selectively affect diseased tissue or cells over normal tissues or cells in the mammalian host. The methods used for binding the cytotoxic agents to the monoclonal antibody molecule can involve either non-covalent or covalent linkages. Since non-covalent bonds are more likely to be broken before the antibody complex reaches the target site, covalent linkages are preferred. For instance, carbodiimide can be used to link
10 carboxy groups of the pharmaceutical agent to amino groups of the antibody molecule. Bifunctional agents such as dialdehydes or imidoesters can be used to link the amino group of a drug to amino groups of the antibody molecule. The Schiff base reaction can be used to link drugs to antibody molecules. This method involves the periodate oxidation of a drug or cytotoxic agent that contains a glycol or hydroxy group, thus forming an aldehyde that is then reacted with the antibody molecule. Attachment occurs via formation of a Schiff base with amino groups of the
15 antibody molecule. Additionally, drugs with reactive sulfhydryl groups have been coupled to antibody molecules.

Example 12 (Diagnostic kit)

Another embodiment of the invention relates to a diagnostic kit for detecting diseased tissue or cells using an antibody against a polypeptide which can mediate signal transduction. The diagnostic kit may further comprise,
20 where necessary, other components of the signal producing system, including agents for reducing background interference, control reagents, or an apparatus, container or other solid support for conducting the test. The binding of antibody to the target can be detected by well known methods, including radiation (*e.g.*, use of a radioactive nucleotide), colorimetry (*e.g.*, use of an enzyme that can cause a color change in a substrate), fluorescence (*e.g.*, use of a dye such as propidium iodide, fluorescein, or rhodamine), and luminescence (*e.g.*, use of an alkaline phosphatase
25 substrate that releases photons upon cleavage or luciferin). Detection can be qualitative or quantitative.

Example 13 (Gene therapy)

Another embodiment of the present invention involves the use of the DNA of the present invention in gene therapy applications. Gene therapy has been broadly defined as "the correction of a disease phenotype through the
30 introduction of new genetic information into the affected organism" (Roemer, K. and Friedmann, T., *Eur. J. Biochem.* 208: 211-225 (1992)). Two basic approaches to gene therapy have evolved: (1) *ex vivo* gene therapy and (2) *in vivo* gene therapy. In *ex vivo* gene therapy, cells are removed from a subject and cultured *in vitro*. A functional replacement gene is introduced into the cells (transfection) *in vitro*, the modified cells are expanded in culture, and then reimplanted in the subject. These genetically modified, reimplanted cells are reported to secrete detectable levels

of the transfected gene product *in situ* (Miller, A.D., *Blood* 76: 271-278 (1990)) and Selden, R.F., *et al.*, *New Eng. J. Med.* 317: 1067-1076 (1987)). The development of improved retroviral gene transfer methods (transduction) facilitates the transfer into and subsequent expression of genetic material by somatic cells (Cepko, C.L., *et al.*, *Cell* 37: 1053-1062 (1984)). Accordingly, retrovirus-mediated gene transfer has been used in clinical trials to mark autologous cells and as a way of treating genetic disease (Rosenberg, S.A., *et al.*, *New Eng. J. Med.* 323: 570-578 (1990); Anderson, W.F., *Human Gene Therapy* 2: 99-100 (1991)). Several *ex vivo* gene therapy studies in humans are reported (reviewed in Anderson, W.F., *Science* 256: 808-813 (1992) and Miller A.D., *Nature* 357: 455-460 (1992)).

In *in vivo* gene therapy, target cells are not removed from the subject. Rather, the transferred gene is introduced into cells of the recipient organism *in situ*, that is, within the recipient. *In vivo* gene therapy has been examined in several animal models (reviewed in Felgner, P.L. and Rhodes, G., *Nature* 349: 351-352 (1991)). Publications have reported the feasibility of direct gene transfer *in situ* into organs and tissues such as muscle (Ferry, N., *et al.*, *Proc. Natl. Acad. Sci.* 88: 8377-8781 (1991); Quantin, G., *et al.*, *Proc. Natl. Acad. Sci. USA* 89: 2581-2584 (1992)), hematopoietic stem cells (Clapp, D.W., *et al.*, *Blood* 78: 1132-1139 (1991)), the arterial wall (Nabel, E.G., *et al.*, *Science* 244: 1342-1344 (1989)), the nervous system (Price, J.D., *et al.*, *Proc. Natl. Acad. Sci.* 84: 156-160 (1987)), and lung (Rosenfeld, M.A., *et al.*, *Science* 252: 431-434 (1991)). Direct injection of DNA into skeletal muscle (Wolff, J.A., *et al.*, *Science* 247: 1465-1468 (1990)), heart muscle (Kitsis, R.N., *et al.*, *Proc. Natl. Acad. Sci. USA* 88: 4138-4142 (1991)) and injection of DNA-lipid complexes into the vasculature (Lim, C.S., *et al.*, *Circulation* 83: 2007-2011 (1991); Ledere, G.D., *et al.*, *J. Clin. Invest.* 90: 936-944 (1992); Chapman, G.D., *et al.*, *Circ. Res.* 71: 27-33 (1992)) also have been reported to yield a detectable expression level of the inserted gene product(s) *in vivo*.

Recent gene therapy efforts have been aimed at the identification of various cell types for transformation, including keratinocytes (Morgan, J.R., *et al.*, *Science* 237: 1476-1479 (1987)), fibroblasts (Palmer, T.D., *et al.*, *Proc. Natl. Acad. Sci.* 88: 1330-1334 (1991); Garver Jr., R.I., *et al.*, *Science* 237: 762-764 (1987); International Patent Application PCT/US92/01890, having publication number WO 92/15676), lymphocytes (Reimann, J.K., *et al.*, *J. Immunol. Methods* 89: 93-101 (1986)), myoblasts (Barr, E. and Leiden, J.M., *Science* 254: 1507-1509 (1991); Dai, Y., *et al.*, *PNAS* 89: 10892-10895 (1992); Roman, M., *et al.*, *Somatic Cell and Molecular Genetics* 18: 247-258 (1992)), smooth muscle cells (Lynch, C.M., *et al.*, *Proc. Natl. Acad. Sci. USA* 89: 1138-1142 (1992)), and epithelial cells (Nabel, E.G., *et al.*, *Science* 244: 1342-1344 (1989)), International Patent Application PCT/US89/05575 (having publication number WO 90/06997), the contents of which references and patent/patent applications are incorporated herein by reference.

The delivery of an effective dose of a prophylactic or therapeutic agent *in situ* depends on the efficiency of transfection (or transduction) as well as the number of target cells. Epithelial cell-based gene therapy, in particular, involves a relatively small area available *in situ* for receiving genetically modified epithelial cells. The delivery of an effective dose of prophylactic or therapeutic agent *in situ* thus depends upon the total number of implanted epithelial cells.

In one embodiment of the invention, exogenous genetic material (*e.g.*, a cDNA encoding a polypeptide of the present invention) is introduced into a syngeneic host cell *ex vivo* or *in vivo* by genetic transfer methods, such as transfection or transduction, to provide a genetically modified host cell. Various expression vectors (*i.e.*, vehicles for facilitating delivery of exogenous genetic material into a target cell) are known to one skilled in the art.

5 Transfection refers to the insertion of nucleic acid into a mammalian host cell using physical or chemical methods. Several transfection techniques are known to those of ordinary skill in the art including: calcium phosphate DNA co-precipitation (METHODS IN MOLECULAR BIOLOGY, Vol. 7, *Gene Transfer and Expression Protocols*, Ed. E.J. Murray, Humana Press (1991)); DEAE-dextran; electroporation; cationic liposome-mediated transfection; and tungsten particle-facilitated microparticle bombardment (Johnston, S.A., *Nature* 346: 776-777 (1990)). Strontium phosphate
10 DNA co-precipitation (Brash D.E. *et al. Molec. Cell. Biol.* 7: 2031-2034 (1987)) is a preferred transfection method.

In contrast, transduction refers to the process of transferring nucleic acid into a cell using a DNA or RNA virus. A RNA virus (*i.e.*, a retrovirus) for transferring a nucleic acid into a cell is referred to herein as a transducing chimeric retrovirus. Exogenous genetic material contained within the retrovirus is incorporated into the genome of the transduced host cell. A host cell that has been transduced with a chimeric DNA virus (*e.g.*, an adenovirus carrying a
15 cDNA encoding a therapeutic agent) will not have the exogenous genetic material incorporated into its genome, but will be capable of expressing the exogenous genetic material that is retained extrachromosomally within the cell.

Typically, the exogenous genetic material includes the heterologous gene (usually in the form of a cDNA comprising the exons coding for the therapeutic protein) together with a promoter to control transcription of the new gene. The promoter characteristically has a specific nucleotide sequence necessary to initiate transcription.
20 Optionally, the exogenous genetic material further includes additional sequences (*i.e.*, enhancers) required to obtain the desired gene transcription activity. For the purpose of this discussion an enhancer is simply any non-translated DNA sequence which works contiguous with the coding sequence (*in cis*) to change the basal transcription level dictated by the promoter. Preferably, the exogenous genetic material is introduced into the host cell genome immediately downstream from the promoter so that the promoter and coding sequence are operatively linked so as to permit
25 transcription of the coding sequence. A preferred retroviral expression vector includes an exogenous promoter element to control transcription of the inserted exogenous gene. Such exogenous promoters include both constitutive and inducible promoters.

Naturally-occurring constitutive promoters control the expression of essential cell functions. As a result, a gene under the control of a constitutive promoter is expressed under all conditions of cell growth. Exemplary
30 constitutive promoters include the promoters for the following genes which encode certain constitutive or housekeeping functions: hypoxanthine phosphoribosyl transferase (HPRT), dihydrofolate reductase (DHFR) (Scharfmann *et al.*, *Proc. Natl. Acad. Sci. USA* 88: 4626-4630 (1991)), adenosine deaminase, phosphoglycerol kinase (PGK), pyruvate kinase, phosphoglycerol mutase, the beta -actin promoter (Lai *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 10006-10010 (1989)), and other constitutive-promoters known to those of skill in the art. In addition, many viral

promoters function constitutively in eukaryotic cells. These include: the early and late promoters of SV40, the long terminal repeats (LTRs) of Moloney Leukemia Virus and other retroviruses, and the thymidine kinase promoter of Herpes Simplex Virus, among many others. Accordingly, any such constitutive promoters can be used to control transcription of a heterologous gene insert.

5 Genes that are under the control of inducible promoters are expressed only or to a greater degree, in the presence of an inducing agent, (*e.g.*, transcription under control of the metallothionein promoter is greatly increased in presence of certain metal ions). Inducible promoters include responsive elements (REs) which stimulate transcription when their inducing factors are bound. For example, there are REs for serum factors, steroid hormones, retinoic acid and cyclic AMP. Promoters containing a particular RE can be chosen in order to obtain an inducible response, and in
10 some cases, the RE itself may be attached to a different promoter, thereby conferring inducibility to the recombinant gene. Thus, by selecting the appropriate promoter (constitutive versus inducible; strong versus weak), it is possible to control both the existence and level of expression of a therapeutic agent in the genetically modified host cell. If the gene encoding the prophylactic or therapeutic agent is under the control of an inducible promoter, delivery of the agent *in situ* is triggered by exposing the genetically modified cell *in situ* to conditions for permitting transcription of the
15 prophylactic or therapeutic agent, *e.g.*, by intraperitoneal injection of specific inducers of the inducible promoters which control transcription of the agent. For example, *in situ* expression by genetically modified host cells of a therapeutic agent encoded by a gene under the control of the metallothionein promoter, is enhanced by contacting the genetically modified cells with a solution containing the appropriate (*i.e.*, inducing) metal ions *in situ*.

Accordingly, the amount of therapeutic agent that is delivered *in situ* is regulated by controlling such factors
20 as: (1) the nature of the promoter used to direct transcription of the inserted gene (*i.e.*, whether the promoter is constitutive or inducible, strong or weak); (2) the number of copies of the exogenous gene that are inserted into the host cell; (3) the number of transduced/transfected host cells that are administered (*e.g.*, implanted) to the patient; (4) the size of the implant (*e.g.*, graft or encapsulated expression system); (5) the number of implants; (6) the length of time the transduced/transfected cells or implants are left in place; and (7) the production rate of the prophylactic or
25 therapeutic agent by the genetically modified host cell. Selection and optimization of these factors for delivery of an effective dose of a particular prophylactic or therapeutic agent is deemed to be within the scope of one of skill in the art, taking into account the above-disclosed factors and the clinical profile of the patient.

In addition to at least one promoter and at least one heterologous nucleic acid encoding the prophylactic or therapeutic agent, the expression vector preferably includes a selection gene, for example, a neomycin resistance
30 gene, for facilitating selection of host cells that have been transfected or transduced with the expression vector. Alternatively, the host cells are transfected with two or more expression vectors, at least one vector containing the gene(s) encoding the prophylactic or therapeutic agent(s), the other vector containing a selection gene. The selection of a suitable promoter, enhancer, selection gene and/or signal sequence is deemed to be within the scope of one skilled in the art.

The prophylactic or therapeutic agent can be targeted for delivery to an extracellular, intracellular or membrane location. If it is desirable for the gene product to be secreted from the host cells, the expression vector is designed to include an appropriate secretion signal sequence for secreting the therapeutic gene product from the cell to the extracellular milieu. If it is desirable for the gene product to be retained within the host cell, this secretion
5 signal sequence is omitted. In a similar manner, the expression vector can be constructed to include retention signal sequences for anchoring the prophylactic or therapeutic agent within the host cell plasma membrane. For example, membrane proteins have hydrophobic transmembrane regions that stop translocation of the protein in the membrane and do not allow the protein to be secreted. The construction of an expression vector including signal sequences for targeting a gene product to a particular location is deemed to be within the scope of one of skill in the art.

10 In an embodiment, vectors for mammalian host cell gene therapy are viruses, more preferably replication-deficient viruses (described in detail below). Exemplary viral vectors are derived from: Harvey Sarcoma Virus; Rous Sarcoma Virus, MPSV, Moloney murine leukemia virus and DNA viruses (*e.g.*, adenovirus). See Temin, H., *Retrovirus vectors for gene transfer*, in GENE TRANSFER, Kucherlapati R, Ed., pp. 149-187 (Plenum 1986).

Replication-deficient retroviruses are capable of directing synthesis of virion proteins, but are incapable of
15 making infectious particles. Accordingly, these genetically altered retroviral expression vectors have general utility for high-efficiency transduction of genes in cultured cells, and specific utility for use in the method of the present invention. Such retroviruses further have utility for the efficient transduction of genes into host cells *in vivo*. Retroviruses have been used extensively for transferring genetic material into cells. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid,
20 transfection of a packaging cell line with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with the viral particles) are provided in Kriegler, M. GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, W.H. Freeman Co., NY (1990) and Murray, E.J., ed. METHODS IN MOLECULAR BIOLOGY, Vol. 7, Humana Press Inc., Clifton, NJ (1991).

The major advantage of using retroviruses for gene therapy is that the viruses insert the gene encoding the
25 therapeutic agent into the host cell genome, thereby permitting the exogenous genetic material to be passed on to the progeny of the cell when it divides. In addition, gene promoter sequences in the LTR region have been reported to enhance expression of an inserted coding sequence in a variety of cell types (*see e.g.*, Hilberg *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 5232-5236 (1987); Holland *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 8662-8666 (1987); Valerio *et al.*, *Gene* 84: 419-427 (1989)). *In vivo* gene therapy using replication-deficient retroviral vectors to deliver a therapeutically
30 effective amount of a therapeutic agent can be efficacious if the efficiency of transduction is high and/or the number of target cells available for transduction is high.

Yet another viral candidate useful as an expression vector for transformation of mammalian host cells is the adenovirus, a double-stranded DNA virus. The adenovirus is frequently responsible for respiratory tract infections in humans and thus appears to have an avidity for the epithelium of the respiratory tract (Straus, S., THE ADENOVIRUS,

5 H.S. Ginsberg, Editor, Plenum Press, NY, p.451-496 (1984)). Moreover, the adenovirus is infective in a wide range of cell types, including, for example, muscle and epithelial cells (Larrick, J.W. and Burck, K.L., GENE THERAPY. APPLICATION OF MOLECULAR BIOLOGY, Elsevier Science Publishing Co., Inc., NY, p.71-104 (1991)). The adenovirus also has been used as an expression vector in muscle cells *in vivo* (Quantin, B., *et al.*, *Proc. Natl. Acad. Sci. USA* 89: 2581-2584 (1992)).

Like the retrovirus, the adenovirus genome is adaptable for use as an expression vector for gene therapy, *i.e.*, by removing the genetic information that controls production of the virus itself (Rosenfeld, M.A., *et al.*, *Science* 252:431-434 (1991)). Because the adenovirus functions in an extrachromosomal fashion, the recombinant adenovirus does not have the theoretical problem of insertional mutagenesis.

10 Thus, as will be apparent to one skilled in the art, a variety of suitable viral expression vectors are available for transferring exogenous genetic material into mammalian host cells. The selection of an appropriate expression vector to express an agent for the identification, prevention or treatment of microbial infection amenable to gene replacement therapy and the optimization of the conditions for insertion of the selected expression vector into the cell are within the scope of one of skill in the art without the need for undue experimentation.

15 In an alternative embodiment, the expression vector is in the form of a plasmid, which is transferred into the target host cells by one of a variety of methods: physical (*e.g.*, microinjection (Capecchi, M.R., *Cell* 22: 479-488 (1980)), electroporation (Andreason, G.L. and Evans, G.A. *Biotechniques* 6: 650-660 (1988)), scrape loading, microparticle bombardment (Johnston, S.A., *Nature* 346: 776-777 (1990)) or by cellular uptake as a chemical complex (*e.g.*, calcium or strontium co-precipitation, complexation with lipid, complexation with ligand) (METHODS IN MOLECULAR
20 BIOLOGY, Vol. 7, GENE TRANSFER AND EXPRESSION PROTOCOLS, Ed. E. J. Murray, Humana Press (1991)). Several commercial products are available for cationic liposome complexation including Lipofectin (Life Technologies, Inc., Gaithersburg, MD) (Felgner, P.L., *et al.*, *Proc. Natl. Acad. Sci.* 84: 7413-7417 (1987)) and Transfectam™ (ProMega, Madison, Wis.) (Behr, J.P., *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 6982-6986 (1989); Loeffler, J.P., *et al.*, *J. Neurochem.* 54: 1812-1815 (1990)). However, the efficiency of transfection by these methods is highly dependent on
25 the nature of the target cell and accordingly, the conditions for optimal transfection of nucleic acids into host cells using the above-mentioned procedures must be optimized. Such optimization is within the scope of one of skill in the art.

In an embodiment, the preparation of genetically modified host cells contains an amount of cells sufficient to deliver a prophylactically or therapeutically effective dose of a signal transduction mediator of the present invention to
30 the recipient *in situ*. The determination of an effective dose of the prophylactic or therapeutic agent for a known microbial infection is within the scope of one of skill in the art. Thus, in determining the effective dose, the skilled artisan would consider the condition of the patient, the severity of the condition, as well as the results of clinical studies of the prophylactic or therapeutic agent being administered.

If the genetically modified host cells are not already present in a pharmaceutically acceptable carrier, they are placed in such a carrier prior to administration to the recipient. Such pharmaceutically acceptable carriers include, for example, isotonic saline and other buffers as appropriate to the patient and therapy. The genetically modified cells are administered by, for example, intraperitoneal injecting or implanting the cells or a graft or capsule containing the cells in a host cell-compatible site of the recipient. As used herein, host cell-compatible site refers to a structure, cavity or fluid of the recipient into which the genetically modified cell(s), host cell graft, or encapsulated host cell expression system can be implanted, without triggering adverse physiological consequences. Representative host cell-compatible sites include, for example, the peritoneal, pleural and pericardial cavities. Preferably, the host cell-compatible site communicates with the lymphatic system, thereby enabling delivery of the therapeutic agent to the vascular system.

In one embodiment, the host cell-compatible site may be denuded prior to implanting the cells. Exemplary denuding methods include but are not limited to: (1) injection of distilled water into the site (*e.g.*, the peritoneal cavity) for 20 minutes, followed by scraping off a portion of the epithelial layer; (2) injection of 0.1% buffered trypsin for 20 minutes followed by scraping; (3) removal of epithelial cells by gentle scraping with a cell scraper and (4) touching a piece of Gelfilm (Upjohn, Kalamazoo, MI) to the endothelium.

The genetically modified host cells are implanted in a host cell-compatible site, alone or in combination with other genetically modified host cells. Thus, the instant invention embraces a method for modifying the epithelial system of a recipient by using a mixture of genetically modified host cells, such that a first modified cell expresses a first prophylactic or therapeutic agent of the present invention and a second modified cell expresses a second prophylactic or therapeutic agent. Other genetically modified cell types (*e.g.*, hepatocytes, smooth muscle cells, fibroblasts, glial cells, mesothelial cells or keratinocytes) can be added, together with the genetically altered epithelial cells, to produce expression of a complex set of introduced genes. Moreover, more than one recombinant gene can be introduced into each genetically modified cell on the same or different vectors, thereby allowing the expression of multiple prophylactic or therapeutic agents of the present invention by a single cell.

The instant invention further embraces an epithelial cell graft. The graft comprises a plurality of the above-described genetically modified cells attached to a support that is suitable for implantation into a mammalian recipient, preferably into the oral cavity. The support can be formed of a natural or synthetic material. According to another aspect of the invention, an encapsulated host cell expression system is provided. The encapsulated system includes a capsule suitable for implantation into a mammalian recipient and a plurality of the above-described genetically modified host cells contained therein. The capsule can be formed of a synthetic or naturally-occurring material. The formulation of such capsules is known to one of ordinary skill in the art. In contrast to the host cells that are directly implanted into the mammalian recipient (*i.e.*, implanted in a manner such that the genetically modified cells are in direct physical contact with the host cell-compatible site), the encapsulated cells remain isolated (*i.e.*, not in direct physical contact with the site) following implantation. Thus, the encapsulated host cell system is not limited to a

capsule including genetically-modified non-immortalized host cells, but may contain genetically modified immortalized host cells.

The invention has been disclosed broadly and illustrated in reference to representative embodiments described above. Those skilled in the art will recognize that various modifications can be made to the present
5 invention without departing from the spirit and scope thereof.

We claim:

1. A purified polypeptide comprising an amino acid sequence having at least 95% sequence identity with sequences selected from the group consisting of SEQ ID NOS: 1, 4, 6, 7, 8 and 9, wherein said polypeptide is capable of regulating signal transduction.
- 5 2. The polypeptide of claim 1, wherein said polypeptide is capable of catalyzing the transfer of a phosphate group from a donor molecule to an acceptor molecule.
3. An isolated DNA molecule encoding the polypeptide of claim 1.
4. An isolated DNA molecule comprising the nucleotide sequence selected from the group consisting of SEQ ID NOS: 2, 3 and 5.
- 10 5. A vector comprising the DNA molecule of claim 3.
6. A host cell transformed with the vector of claim 5.
7. The host cell of claim 6, wherein said host cell produces a polypeptide capable of regulating signal transduction.
8. The host cell of claim 6, wherein said host cell produces a polypeptide capable of catalyzing the transfer
15 of a phosphate group from a donor molecule to an acceptor molecule.
9. An isolated antibody against the polypeptide of claim 1.
10. The antibody of claim 9, wherein said antibody is a monoclonal antibody.
11. The antibody of claim 9, wherein said antibody is capable of inhibiting the regulation of signal transduction.
- 20 12. The antibody of claim 9, wherein said antibody is capable of inhibiting the transfer of a phosphate group from a donor molecule to an acceptor molecule.
13. An isolated nucleic acid capable of hybridizing under high stringency conditions to the DNA molecule of claim 3.
14. The isolated nucleic acid of claim 13, wherein said nucleic acid is capable of inhibiting the regulation of
25 signal transduction.
15. The isolated nucleic acid of claim 13, wherein said nucleic acid is capable of inhibiting said transfer of said phosphate group from said donor molecule to said acceptor molecule.
16. A method of preventing or treating disease in a mammal comprising administering to said mammal an effective amount of material, selected from the group consisting of the polypeptide of claim 1 and antibody against
30 said polypeptide, in a pharmaceutically acceptable sterile vehicle.
17. The method of claim 16, wherein said mammal is a human.
18. The method of claim 16, wherein said disease is cardiac disease.

19. A vaccine for preventing disease in a mammal comprising administering to said mammal an effective amount of material, selected from the group consisting of the polypeptide of claim 1 and the antibody against said polypeptide, in a pharmaceutically acceptable sterile vehicle.

20. The vaccine of claim 19, wherein said mammal is a human.

5 21. The vaccine of claim 19, wherein said disease is cardiac disease.

22. A method of preventing or treating disease in a mammal comprising administering to said mammal syngeneic cells transformed with the vector of claim 5, wherein said transformed syngeneic cells produce a polypeptide capable of regulating signal transduction.

23. The method of claim 22, wherein said mammal is a human.

10 24. The method of claim 22, wherein said disease is cardiac disease.

25. A method of preventing or treating disease in a mammal comprising administering to said mammal syngeneic cells transformed with the vector of claim 5, wherein said transformed syngeneic cells produce a polypeptide capable of catalyzing the transfer of a phosphate group from a donor molecule to an acceptor molecule.

26. The method of claim 25, wherein said mammal is a human.

15 27. The method of claim 25, wherein said disease is cardiac disease.

28. A kit for detecting the expression of a protein capable of regulating signal transduction, comprising the polypeptide of claim 1.

29. The kit of claim 28, further comprising a detectable label selected from the group consisting of colorimetric, enzymatic, chemiluminescent, fluorescent and radioactive labels.

20 30. A kit for detecting the expression of a protein capable of acting as a donor molecule or an acceptor molecule of a phosphate group, comprising the polypeptide of claim 1.

31. The kit of claim 30, further comprising a detectable label selected from the group consisting of colorimetric, enzymatic, chemiluminescent, fluorescent and radioactive labels.

25 32. A method for detecting the expression of a protein capable of regulating signal transduction, comprising contacting a sample with the polypeptide of claim 1, and detecting any effect of the sample on an indicator of signal transduction.

33. The method of claim 32, wherein said polypeptide is immobilized to a solid support.

34. The method of claim 32, wherein said phosphate group is detectably labeled.

30 35. A method for detecting the expression of a protein capable of acting as a donor molecule or an acceptor molecule of a phosphate group, comprising contacting a sample with the polypeptide of claim 1, and detecting any transfer of said phosphate group.

36. The method of claim 35, wherein said polypeptide is immobilized to a solid support.

37. The method of claim 35, wherein said phosphate group is detectably labeled.

SEQUENCE LISTING

<110> Wenlin Zeng
Lawrence Stanton

<120> Mediators of signal transduction

<130> SCIOS.021A

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1351

<212> PRT

<213> Homo sapiens

<400> 1

Gly	Val	Gln	Phe	Ser	Gln	Tyr	Gly	Ser	Pro	Glu	Phe	Val	Ser	Pro	Glu	1	5	10	15
Ile	Ile	Gln	Gln	Asn	Pro	Val	Ser	Glu	Ala	Ser	Asp	Ile	Trp	Ala	Met	20	25	30	
Gly	Val	Ile	Ser	Tyr	Leu	Ser	Leu	Thr	Cys	Ser	Ser	Pro	Phe	Ala	Gly	35	40	45	
Glu	Ser	Asp	Arg	Ala	Thr	Leu	Leu	Asn	Val	Leu	Glu	Gly	Arg	Val	Ser	50	55	60	
Trp	Ser	Ser	Pro	Met	Ala	Ala	His	Leu	Ser	Glu	Asp	Ala	Lys	Asp	Phe	65	70	75	80
Ile	Lys	Ala	Thr	Leu	Gln	Arg	Ala	Pro	Gln	Ala	Arg	Pro	Ser	Ala	Ala	85	90	95	
Gln	Cys	Leu	Ser	His	Pro	Trp	Phe	Leu	Lys	Ser	Met	Pro	Ala	Glu	Glu	100	105	110	
Ala	His	Phe	Ile	Asn	Thr	Lys	Gln	Leu	Lys	Phe	Leu	Leu	Ala	Arg	Ser	115	120	125	
Arg	Trp	Gln	Arg	Ser	Leu	Met	Ser	Tyr	Lys	Ser	Ile	Leu	Val	Met	Arg	130	135	140	
Ser	Ile	Pro	Glu	Leu	Leu	Arg	Gly	Pro	Pro	Asp	Ser	Pro	Ser	Leu	Gly	145	150	155	160
Val	Ala	Arg	His	Leu	Cys	Arg	Asp	Thr	Gly	Gly	Ser	Ser	Ser	Ser	Ser	165	170	175	
Ser	Ser	Ser	Asp	Asn	Glu	Leu	Ala	Pro	Phe	Ala	Arg	Ala	Lys	Ser	Leu	180	185	190	
Pro	Pro	Ser	Pro	Val	Thr	His	Ser	Pro	Leu	Leu	His	Pro	Arg	Gly	Phe	195	200	205	
Leu	Arg	Pro	Ser	Ala	Ser	Leu	Pro	Glu	Glu	Ala	Glu	Ala	Ser	Glu	Arg	210	215	220	
Ser	Thr	Glu	Ala	Pro	Ala	Pro	Pro	Ala	Ser	Pro	Glu	Gly	Ala	Gly	Pro	225	230	235	240
Pro	Ala	Ala	Gln	Gly	Cys	Val	Pro	Arg	His	Ser	Val	Ile	Arg	Ser	Leu	245	250	255	
Phe	Tyr	His	Gln	Ala	Gly	Glu	Ser	Pro	Glu	His	Gly	Ala	Leu	Ala	Pro	260	265	270	

Gly Ser Arg Arg His Pro Ala Arg Arg Arg His Leu Leu Lys Gly Gly
 275 280 285
 Tyr Ile Ala Gly Ala Leu Pro Gly Leu Arg Glu Pro Leu Met Glu His
 290 295 300
 Arg Val Leu Glu Glu Glu Ala Ala Arg Glu Glu Gln Ala Thr Leu Leu
 305 310 315 320
 Ala Lys Ala Pro Ser Phe Glu Thr Ala Leu Arg Leu Pro Ala Ser Gly
 325 330 335
 Thr His Leu Ala Pro Gly His Ser His Ser Leu Glu His Asp Ser Pro
 340 345 350
 Ser Thr Pro Arg Pro Ser Ser Glu Ala Cys Gly Glu Ala Gln Arg Leu
 355 360 365
 Pro Ser Ala Pro Ser Gly Gly Ala Pro Ile Arg Asp Met Gly His Pro
 370 375 380
 Gln Gly Ser Lys Gln Leu Pro Ser Thr Gly Gly His Pro Gly Thr Ala
 385 390 395 400
 Gln Pro Glu Arg Pro Ser Pro Asp Ser Pro Trp Gly Gln Pro Ala Pro
 405 410 415
 Phe Cys His Pro Lys Gln Gly Ser Ala Pro Gln Glu Gly Cys Ser Pro
 420 425 430
 His Pro Ala Val Ala Pro Cys Pro Gly Ser Phe Pro Pro Gly Ser
 435 440 445
 Cys Lys Glu Ala Pro Leu Val Pro Ser Ser Pro Phe Leu Gly Gln Pro
 450 455 460
 Gln Ala Pro Pro Ala Pro Ala Lys Ala Ser Pro Pro Leu Asp Ser Lys
 465 470 475 480
 Met Gly Pro Gly Asp Ile Ser Leu Pro Gly Arg Pro Lys Pro Gly Pro
 485 490 495
 Cys Ser Ser Pro Gly Ser Ala Ser Gln Ala Ser Ser Ser Gln Val Ser
 500 505 510
 Ser Leu Arg Val Gly Ser Ser Gln Val Gly Thr Glu Pro Gly Pro Ser
 515 520 525
 Leu Asp Ala Glu Gly Trp Thr Gln Glu Ala Glu Asp Leu Ser Asp Ser
 530 535 540
 Thr Pro Thr Leu Gln Arg Pro Gln Glu Gln Ala Thr Met Arg Lys Phe
 545 550 555 560
 Ser Leu Gly Gly Arg Gly Gly Tyr Ala Gly Val Ala Gly Tyr Gly Thr
 565 570 575
 Phe Ala Phe Gly Gly Asp Ala Gly Gly Met Leu Gly Gln Gly Pro Met
 580 585 590
 Trp Ala Arg Ile Ala Trp Ala Val Ser Gln Ser Glu Glu Glu Glu Gln
 595 600 605
 Glu Glu Ala Arg Ala Glu Ser Gln Ser Glu Glu Gln Gln Glu Ala Arg
 610 615 620
 Ala Glu Ser Pro Leu Pro Gln Val Ser Ala Arg Pro Val Pro Glu Val
 625 630 635 640
 Gly Arg Ala Pro Thr Arg Ser Ser Pro Glu Pro Thr Pro Trp Glu Asp
 645 650 655
 Ile Gly Gln Val Ser Leu Val Gln Ile Arg Asp Leu Ser Gly Asp Ala
 660 665 670
 Glu Ala Ala Asp Thr Ile Ser Leu Asp Ile Ser Glu Val Asp Pro Ala
 675 680 685
 Tyr Leu Asn Leu Ser Asp Leu Tyr Asp Ile Lys Tyr Leu Pro Phe Glu
 690 695 700
 Phe Met Ile Phe Arg Lys Val Pro Lys Ser Ala Gln Pro Glu Pro Pro
 705 710 715 720
 Ser Pro Met Ala Glu Glu Glu Leu Ala Glu Phe Pro Glu Pro Thr Trp

Pro	Trp	Pro	Gly	725	Glu	Leu	Gly	Pro	His	Ala	Gly	Leu	Glu	Ile	Thr	Glu	735
			740						745					750			
Glu	Ser	Glu	Asp	Val	Asp	Ala	Leu	Leu	Ala	Glu	Ala	Ala	Val	Gly	Arg		
		755					760					765					
Lys	Arg	Lys	Trp	Ser	Ser	Pro	Ser	Arg	Ser	Leu	Phe	His	Phe	Pro	Gly		
		770					775				780						
Arg	His	Leu	Pro	Leu	Asp	Glu	Pro	Ala	Glu	Leu	Gly	Leu	Arg	Glu	Arg		
785					790					795					800		
Val	Lys	Ala	Ser	Val	Glu	His	Ile	Ser	Arg	Ile	Leu	Lys	Gly	Arg	Pro		
				805					810					815			
Glu	Gly	Leu	Glu	Lys	Glu	Gly	Pro	Pro	Arg	Lys	Lys	Pro	Gly	Leu	Ala		
			820					825					830				
Ser	Phe	Arg	Leu	Ser	Gly	Leu	Lys	Ser	Trp	Asp	Arg	Ala	Pro	Thr	Phe		
		835					840					845					
Leu	Arg	Glu	Leu	Ser	Asp	Glu	Thr	Val	Val	Leu	Gly	Gln	Ser	Val	Thr		
		850				855					860						
Leu	Ala	Cys	Gln	Val	Ser	Ala	Gln	Pro	Ala	Ala	Gln	Ala	Thr	Trp	Ser		
865					870					875					880		
Lys	Asp	Gly	Ala	Pro	Leu	Glu	Ser	Ser	Ser	Arg	Val	Leu	Ile	Ser	Ala		
				885					890					895			
Thr	Leu	Lys	Asn	Phe	Gln	Leu	Leu	Thr	Ile	Leu	Val	Val	Val	Ala	Glu		
			900					905					910				
Asp	Leu	Gly	Val	Tyr	Thr	Cys	Ser	Val	Ser	Asn	Ala	Leu	Gly	Thr	Val		
		915					920					925					
Thr	Thr	Thr	Gly	Val	Leu	Arg	Lys	Ala	Glu	Arg	Pro	Ser	Ser	Ser	Pro		
		930				935					940						
Cys	Pro	Asp	Ile	Gly	Glu	Val	Tyr	Ala	Asp	Gly	Val	Leu	Leu	Val	Trp		
945					950					955					960		
Lys	Pro	Val	Glu	Ser	Tyr	Gly	Pro	Val	Thr	Tyr	Ile	Val	Gln	Cys	Ser		
				965					970					975			
Leu	Glu	Gly	Gly	Ser	Trp	Thr	Thr	Leu	Ala	Ser	Asp	Ile	Phe	Asp	Cys		
			980					985					990				
Cys	Tyr	Leu	Thr	Ser	Lys	Leu	Ser	Arg	Gly	Gly	Thr	Tyr	Thr	Phe	Arg		
		995					1000					1005					
Thr	Ala	Cys	Val	Ser	Lys	Ala	Gly	Met	Gly	Pro	Tyr	Ser	Ser	Pro	Ser		
		1010				1015					1020						
Glu	Gln	Val	Leu	Leu	Gly	Gly	Pro	Ser	His	Leu	Ala	Ser	Glu	Glu	Glu		
1025					1030					1035					1040		
Ser	Gln	Gly	Arg	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Thr	Lys	Thr	Phe	Ala		

Tyr Asn Leu Leu Lys Val Val Asp Leu Gly Asn Ala Gln Ser Leu Ser
 1185 1190 1195 1200
 Gln Glu Lys Val Leu Pro Ser Asp Lys Phe Lys Asp Tyr Leu Glu Thr
 1205 1210 1215
 Met Ala Pro Glu Leu Leu Glu Gly Gln Gly Ala Val Pro Gln Thr Asp
 1220 1225 1230
 Ile Trp Ala Ile Gly Val Thr Ala Phe Ile Met Leu Ser Ala Glu Tyr
 1235 1240 1245
 Pro Val Ser Ser Glu Gly Ala Arg Asp Leu Gln Arg Gly Leu Arg Lys
 1250 1255 1260
 Gly Leu Val Arg Leu Ser Arg Cys Tyr Ala Gly Leu Ser Gly Gly Ala
 1265 1270 1275 1280
 Val Ala Phe Leu Arg Ser Thr Leu Cys Ala Gln Pro Trp Gly Arg Pro
 1285 1290 1295
 Cys Ala Ser Ser Cys Leu Gln Cys Pro Trp Leu Thr Glu Glu Gly Pro
 1300 1305 1310
 Ala Cys Ser Arg Pro Ala Pro Val Thr Phe Pro Thr Ala Arg Leu Arg
 1315 1320 1325
 Val Phe Val Arg Asn Arg Glu Lys Arg Arg Ala Leu Leu Tyr Lys Arg
 1330 1335 1340
 His Asn Leu Ala Gln Val Arg
 1345 1350

<210> 2
 <211> 4175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(4053)

<400> 2
 gga gtg cag ttc agc cag tac ggc tcc cct gag ttc gtc tcc ccc gag 48
 atc atc cag cag aac cct gtg agc gaa gcc tcc gac att tgg gcc atg 96
 ggt gtc atc tcc tac ctc agc ctg acc tgc tca tcc cca ttt gcc ggc 144
 gag agt gac cgt gcc acc ctc ctg aac gtc ctg gag ggg cgc gtg tca 192
 tgg agc agc ccc atg gct gcc cac ctc agc gaa gac gcc aaa gac ttc 240
 atc aag gct acg ctg cag aga gcc cct cag gcc cgg cct agt gcg gcc 288
 cag tgc ctc tcc cac ccc tgg ttc ctg aaa tcc atg cct gcg gag gag 336
 gcc cac ttc atc aac acc aag cag ctc aag ttc ctc ctg gcc cga agt 384
 cgc tgg cag cgt tcc ctg atg agc tac aag tcc atc ctg gtg atg cgc 432
 tcc atc cct gag ctg ctg cgg ggc cca ccc gac agc ccc tcc ctc ggc 480
 gta gcc cgg cac ctc tgc agg gac act ggt ggc tcc tcc agt tcc tcc 528
 tcc tcc tct gac aac gag ctc gcc cca ttt gcc cgg gct aag tca ctg 576
 cca ccc tcc ccg gtg aca cac tca cca ctg ctg cac ccc cgg ggc ttc 624
 ctg cgg ccc tcc gcc agc ctg cct gag gaa gcc gag gcc agt gag cgc 672
 tcc acc gag gcc cca gct ccg cct gca tct ccc gag ggt gcc ggg cca 720
 ccg gcc gcc cag ggc tgc gtg ccc cgg cac agc gtc atc cgc agc ctg 768
 ttc tac cac cag gcg ggt gag agc cct gag cac ggg gcc ctg gcc ccg 816
 ggg agc agg cgg cac ccg gcc cgg cgg cgg cac ctg ctg aag ggc ggg 864
 tac att gcg ggg gcg ctg cca ggc ctg cgc gag cca ctg atg gag cac 912
 cgc gtg ctg gag gag gag gcc gcc .agg gag gag cag gcc acc ctc ctg 960

gcc	aaa	gcc	ccc	tca	ttc	gag	act	gcc	ctc	cgg	ctg	cct	gcc	tct	ggc	1008
acc	cac	ttg	gcc	cct	ggc	cac	agc	cac	tcc	ctg	gaa	cat	gac	tct	cgc	1056
agc	acc	ccc	cgc	ccc	tcc	tcg	gag	gcc	tgc	ggt	gag	gca	cag	cga	ctg	1104
cct	tca	gcc	ccc	tcc	ggg	ggg	gcc	cct	atc	agg	gac	atg	ggg	cac	cct	1152
cag	ggc	tcc	aag	cag	ctt	cca	tcc	act	ggt	ggc	cac	cca	ggc	act	gct	1200
cag	cca	gag	agg	cca	tcc	ccg	gac	agc	cct	tgg	ggg	cag	cca	gcc	cct	1248
ttc	tgc	cac	ccc	aag	cag	ggt	tct	gcc	ccc	cag	gag	ggc	tgc	agc	ccc	1296
cac	cca	gca	gtt	gcc	cca	tgc	cct	cct	ggc	tcc	ttc	cct	cca	gga	tct	1344
tgc	aaa	gag	gcc	ccc	tta	gta	ccc	tca	agc	ccc	ttc	ttg	gga	cag	ccc	1392
cag	gca	ccc	cct	gcc	cct	gcc	aaa	gca	agc	ccc	cca	ttg	gac	tct	aag	1440
atg	ggg	cct	gga	gac	atc	tct	ctt	cct	ggg	agg	cca	aaa	ccc	ggc	ccc	1488
tgc	agt	tcc	cca	ggg	tca	gcc	tcc	cag	gcg	agc	tct	tcc	caa	gtg	agc	1536
tcc	ctc	agg	gtg	ggc	tcc	tcc	cag	gtg	ggc	aca	gag	cct	ggc	ccc	tcc	1584
ctg	gat	gcg	gag	ggc	tgg	acc	cag	gag	gct	gag	gat	ctg	tcc	gac	tcc	1632
aca	ccc	acc	ttg	cag	cgg	cct	cag	gaa	cag	gcg	acc	atg	cgc	aag	ttc	1680
tcc	ctg	ggt	ggt	cgc	ggg	ggc	tac	gca	ggc	gtg	gct	ggc	tat	ggc	acc	1728
ttt	gcc	ttt	ggt	gga	gat	gca	ggg	ggc	atg	ctg	ggg	cag	ggg	ccc	atg	1776
tgg	gcc	agg	ata	gcc	tgg	gct	gtg	tcc	cag	tca	gag	gag	gag	gag	cag	1824
gag	gag	gcc	agg	gct	gag	tcc	cag	tcg	gag	gag	cag	cag	gag	gcc	agg	1872
gct	gag	agc	cca	ctg	ccc	cag	gtc	agt	gca	agg	cct	gtg	cct	gag	gtc	1920
ggc	agg	gct	ccc	acc	agg	agc	tct	cca	gag	ccc	acc	cca	tgg	gag	gac	1968
atc	ggg	cag	gtc	tcc	ctg	gtg	cag	atc	cgg	gac	ctg	tca	ggt	gat	gcg	2016
gag	gcg	gcc	gac	aca	ata	tcc	ctg	gac	att	tcc	gag	gtg	gac	ccc	gcc	2064
tac	ctc	aac	ctc	tca	gac	ctg	tac	gat	atc	aag	tac	ctc	cca	ttc	gag	2112
ttt	atg	atc	ttc	agg	aaa	gtc	ccc	aag	tcc	gct	cag	cca	gag	ccg	ccc	2160
tcc	ccc	atg	gct	gag	gag	gag	ctg	gcc	gag	ttc	ccg	gag	ccc	acg	tgg	2208
ccc	tgg	cca	ggt	gaa	ctg	ggc	ccc	cac	gca	ggc	ctg	gag	atc	aca	gag	2256
gag	tca	gag	gat	gtg	gac	gcg	ctg	ctg	gca	gag	gct	gcc	gtg	ggc	agg	2304
aag	cgc	aag	tgg	tcc	tcg	ccg	tca	cgc	agc	ctc	ttc	cac	ttc	cct	ggg	2352
agg	cac	ctg	ccg	ctg	gat	gag	cct	gca	gag	ctg	ggg	ctg	cgt	gag	aga	2400
gtg	aag	gcc	tcc	gtg	gag	cac	atc	tcc	cgg	atc	ctg	aag	ggc	agg	ccg	2448
gaa	ggt	ctg	gag	aag	gag	ggg	ccc	ccc	agg	aag	aag	cca	ggc	ctt	gct	2496
tcc	ttc	cgg	ctc	tca	ggt	ctg	aag	agc	tgg	gac	cga	gcg	ccg	aca	ttc	2544
cta	agg	gag	ctc	tca	gat	gag	act	gtg	gtc	ctg	ggc	cag	tca	gtg	aca	2592
ctg	gcc	tgc	cag	gtg	tca	gcc	cag	cca	gct	gcc	cag	gcc	acc	tgg	agc	2640
aaa	gac	gga	gcc	ccc	ctg	gag	agc	agc	agc	cgt	gtc	ctc	atc	tct	gcc	2688
acc	ctc	aag	aac	ttc	cag	ctt	ctg	acc	atc	ctg	gtg	gtg	gtg	gct	gag	2736
gac	ctg	ggt	gtg	tac	acc	tgc	agc	gtg	agc	aat	gcg	ctg	ggg	aca	gtg	2784
acc	acc	acg	ggc	gtc	ctc	cgg	aag	gca	gag	cgc	ccc	tca	tct	tcg	cca	2832
tgc	ccg	gat	atc	ggg	gag	gtg	tac	gcg	gat	ggg	gtg	ctg	ctg	gtc	tgg	2880
aag	ccc	gtg	gaa	tcc	tac	ggc	cct	gtg	acc	tac	att	gtg	cag	tgc	agc	2928
cta	gaa	ggc	ggc	agc	tgg	acc	aca	ctg	gcc	tcc	gac	atc	ttt	gac	tgc	2976
tgc	tac	ctg	acc	agc	aag	ctc	tcc	cgg	ggt	ggc	acc	tac	acc	ttc	cgc	3024
acg	gca	tgt	gtc	agc	aag	gca	gga	atg	ggt	ccc	tac	agc	agc	ccc	tcg	3072
gag	caa	gtc	ctc	ctg	gga	ggg	ccc	agc	cac	ctg	gcc	tct	gag	gag	gag	3120
agc	cag	ggg	cgg	tca	gcc	caa	ccc	ctg	ccc	agc	aca	aag	acc	ttc	gca	3168
ttc	cag	aca	cag	atc	cag	agg	ggc	cgc	ttc	agc	gtg	gtg	cgg	caa	tgc	3216
tgg	gag	aag	gcc	agc	ggg	cgg	gcg	ctg	gcc	gcc	aag	atc	atc	ccc	tac	3264
cac	ccc	aag	gac	aag	aca	gca	gtg	ctg	cgc	gaa	tac	gag	gcc	ctc	aag	3312
ggc	ctg	cgc	cac	ccg	cac	ctg	gcc	cag	ctg	cac	gca	gcc	tac	ctc	agc	3360
ccc	cgg	cac	ctg	gtg	ctc	atc	ttg	gag	ctg	tgc	tct	ggg	ccc	gag	ctg	3408
ctc	ccc	tgc	ctg	gcc	gag	agg	gcc	tcc	tac	tca	gaa	tcc	gag	gtg	aag	3456
gac	tac	ctg	tgg	cag	atg	ttg	agt	gcc	acc	cag	tac	ctg	cac	aac	cag	3504
cac	atc	ctg	cac	ctg	gac	ctg	agg	tcc	gag	aac	atg	atc	atc	acc	gaa	3552
tac	aac	ctg	ctc	aag	gtc	gtg	gac	ctg	ggc	aat	gca	cag	agc	ctc	agc	3600
cag	gag	aag	gtg	ctg	ccc	tca	gac	aag	ttc	aag	gac	tac	cta	gag	acc	3648
atg	gct	cca	gag	ctc	ctg	gag	ggc	cag	ggg	gct	gtt	cca	cag	aca	gac	3696

```

atc tgg gcc atc ggt gtg aca gcc ttc atc atg ctg agc gcc gag tac 3744
ccg gtg agc agc gag ggt gca cgc gac ctg cag aga gga ctg cgc aag 3792
ggg ctg gtc cgg ctg agc cgc tgc tac gcg ggg ctg tcc ggg ggc gcc 3840
gtg gcc ttc ctg cgc agc act ctg tgc gcc cag ccc tgg ggc cgc ccc 3888
tgc gcg tcc agc tgc ctg cag tgc ccg tgg cta aca gag gag ggc ccg 3936
gcc tgt tgc cgg ccc gcg ccc gtg acc ttc cct acc gcg cgc ctg cgc 3984
gtc ttc gtg cgc aat cgc gag aag aga cgc gcg ctg ctg tac aag agg 4032
cac aac ctg gcc cag gtg cgc tgagggtcgc ccgcggccaca cccttggtct 4083
ccccgtggg ggtcgtgca gacgcgcaa taaaaacgca cagccgggcg agaaaaaaaa 4143
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 4175

```

```

<210> 3
<211> 5007
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (97)...(4926)

```

```

<400> 3
ctgctctggg acgtccacag ccacgtggtc agagagacca cacagaggac ctacacatac 60
caggccatcg acacgcacac cgcacggccc ccatcc atg cag gta acc atc gag 114
gat gtg cag gca cag aca ggc gga acg gcc caa ttc gag gct atc att 162
gag ggc gac cca cag ccc tgc gtg acc tgg tac aag gac agc gtc cag 210
ctg gtg gac agc acc cgg ctt agc cag cag caa gaa ggc acc aca tac 258
tcc ctg gtg ctg agg cat gtg gcc tgc aag gat gcc ggc gtt tac acc 306
tgc ctg gcc caa aac act ggt ggc cag gtg ctc tgc aag gca gag ctg 354
ctg gtg ctt ggg ggc gac aat gag cgc gac tca gag aag caa agc cac 402
cgg agg aag ctg cac tcc ttc tat gag gtc aag gag gag att gga agg 450
ggc gtg ttt ggc ttc gta aaa aga gtg cag cac aaa gga aac aag atc 498
ttg tgc gct gcc aag ttc atc ccc cta cgg agc aga act cgg gcc cag 546
gca tac agg gag cga gac atc ctg gcc gcg ctg agc cac ccg ctg gtc 594
acg ggg ctg ctg gac cag ttt gag acc cgc aag acc ctc atc ctc atc 642
ctg gag ctg tgc tca tcc gag gag ctg ctg gac cgc ctg tac agg aag 690
ggc gtg gtg acg gag gcc gag gtc aag gtc tac atc cag cag ctg gtg 738
gag ggg ctg cac tac ctg cac agc cat ggc gtt ctc cac ctg gac ata 786
aag ccc tct aac atc ctg atg gtg cat cct gcc cgg gaa gac att aaa 834
atc tgc gac ttt ggc ttt gcc cag aac atc acc cca gca gag ctg cag 882
ttc agc cag tac ggc tcc cct gag ttc gtc tcc ccc gag atc atc cag 930
cag aac cct gtg agc gaa gcc tcc gac att tgg gcc atg ggt gtc atc 978
tcc tac ctc agc ctg acc tgc tca tcc cca ttt gcc ggc gag agt gac 1026
cgt gcc acc ctc ctg aac gtc ctg gag ggg cgc gtg tca tgg agc agc 1074
ccc atg gct gcc cac ctc agc gaa gac gcc aaa gac ttc atc aag gct 1122
acg ctg cag aga gcc cct cag gcc cgg cct agt gcg gcc cag tgc ctc 1170
tcc cac ccc tgg ttc ctg aaa tcc atg cct gcg gag gag gcc cac ttc 1218
atc aac acc aag cag ctc aag ttc ctc ctg gcc cga agt cgc tgg cag 1266
cgt tcc ctg atg agc tac aag tcc atc ctg gtg atg cgc tcc atc cct 1314
gag ctg ctg cgg ggc cca ccc gac agc ccc tcc ctc ggc gta gcc cgg 1362
cac ctc tgc agg gac act ggt ggc tcc tcc agt tcc tcc tcc tcc tct 1410
gac aac gag ctc gcc cca ttt gcc cgg gct aag tca ctg cca ccc tcc 1458
ccg gtg aca cac tca cca ctg ctg cac ccc cgg ggc ttc ctg cgg ccc 1506

```

tcg gcc agc ctg cct gag gaa gcc gag gcc agt gag cgc tcc acc gag	1554
gcc cca gct ccg cct gca tct ccc gag ggt gcc ggg cca ccg gcc gcc	1602
cag ggc tgc gtg ccc cgg cac agc gtc atc cgc agc ctg ttc tac cac	1650
cag gcg ggt gag agc cct gag cac ggg gcc ctg gcc ccg ggg agc agg	1698
cgg cac ccg gcc cgg cgg cgg cac ctg ctg aag ggc ggg tac att gcg	1746
ggg gcg ctg cca ggc ctg cgc gag cca ctg atg gag cac cgc gtg ctg	1794
gag gag gag gcc gcc agg gag gag cag gcc acc ctg gcc aaa gcc	1842
ccc tca ttc gag act gcc ctg cgg ctg cct gcc tct ggc acc cac ttg	1890
gcc cct ggc cac agc cac tcc ctg gaa cat gac tct ccg agc acc ccc	1938
cgc ccc tcc tcg gag gcc tgc ggt gag gca cag cga ctg cct tca gcc	1986
ccc tcc ggg ggg gcc cct atc agg gac atg ggg cac cct cag ggc tcc	2034
aag cag ctt cca tcc act ggt ggc cac cca ggc act gct cag cca gag	2082
agg cca tcc ccg gag agc cct tgg ggg cag cca gcc cct ttc tgc cac	2130
ccc aag cag ggt tct gcc ccc cag gag ggc tgc agc ccc cac cca gca	2178
ggt gcc cca tgc cct cct ggc tcc ttc cct cca gga tct tgc aaa gag	2226
gcc ccc tta gta ccc tca agc ccc ttc ttg gga cag ccc cag gca ccc	2274
cct gcc cct gcc aaa gca agc ccc cca ttg gac tct aag atg ggg cct	2322
gga gac atc tct ctt cct ggg agg cca aaa ccc ggc ccc tgc agt tcc	2370
cca ggg tca gcc tcc cag gcg agc tct tcc caa gtg agc tcc ctg agg	2418
gtg ggc tcc tcc cag gtg ggc aca gag cct ggc ccc tcc ctg gat gcg	2466
gag ggc tgg acc cag gag gct gag gat ctg tcc gac tcc aca ccc acc	2514
ttg cag cgg cct cag gaa cag gcg acc atg cgc aag ttc tcc ctg ggt	2562
ggt cgc ggg ggc tac gca ggc gtg gct ggc tat ggc acc ttt gcc ttt	2610
ggt gga gat gca ggg ggc atg ctg ggg cag ggg ccc atg tgg gcc agg	2658
ata gcc tgg gct gtg tcc cag tca gag gag gag gag cag gag gag gcc	2706
agg gct gag tcc cag tcg gag gag cag gag gcc agg gct gag agc	2754
cca ctg ccc cag gtc agt gca agg cct gtg cct gag gtc ggc agg gct	2802
ccc acc agg agc tct cca gag ccc acc cca tgg gag gac atc ggg cag	2850
gtc tcc ctg gtg cag atc cgg gac ctg tca ggt gat gcg gag gcg gcc	2898
gac aca ata tcc ctg gac att tcc gag gtg gac ccc gcc tac ctg aac	2946
ctc tca gac ctg tac gat atc aag tac ctg cca ttc gag ttt atg atc	2994
ttc agg aaa gtc ccc aag tcc gct cag cca gag ccg ccc tcc ccc atg	3042
gct gag gag gag ctg gcc gag ttc ccg gag ccc acc tgg ccc tgg cca	3090
ggt gaa ctg ggc ccc cac gca ggc ctg gag atc aca gag gag tca gag	3138
gat gtg gac gcg ctg ctg gca gag gct gcc gtg ggc agg aag cgc aag	3186
tgg tcc tcg ccg tca cgc agc ctg ttc cac ttc cct ggg agg cac ctg	3234
ccg ctg gat gag cct gca gag ctg ggg ctg cgt gag aga gtg aag gcc	3282
tcc gtg gag cac atc tcc cgg atc ctg aag ggc agg ccg gaa ggt ctg	3330
gag aag gag ggg ccc ccc agg aag aag cca ggc ctt gct tcc ttc cgg	3378
ctc tca ggt ctg aag agc tgg gac cga gcg ccg aca ttc cta agg gag	3426
ctc tca gat gag act gtg gtc ctg ggc cag tca gtg aca ctg gcc tgc	3474
cag gtg tca gcc cag cca gct gcc cag gcc acc tgg agc aaa gac gga	3522
gcc ccc ctg gag agc agc agc cgt gtc ctg atc tct gcc acc ctg aag	3570
aac ttc cag ctt ctg acc atc ctg gtg gtg gtg gct gag gac ctg ggt	3618
gtg tac acc tgc agc gtg agc aat gcg ctg ggg aca gtg acc acc acg	3666
ggc gtc ctg cgg aag gca gag cgc ccc tca tct tcg cca tgc ccg gat	3714
atc ggg gag gtg tac gcg gat ggg gtg ctg ctg gtc tgg aag ccc gtg	3762
gaa tcc tac ggc cct gtg acc tac att gtg cag tgc agc cta gaa ggc	3810
ggc agc tgg acc aca ctg gcc tcc gac atc ttt gac tgc tgc tac ctg	3858
acc agc aag ctg tcc cgg ggt ggc acc tac acc ttc cgc acg gca tgt	3906
gtc agc aag gca gga atg ggt ccc tac agc agc ccc tcg gag caa gtc	3954
ctc ctg gga gcg ccc agc cac ctg gcc tct gag gag gag agc cag ggg	4002
cgg tca gcc caa ccc ctg ccc agc aca aag acc ttc gca ttc cag aca	4050
cag atc cag agg ggc cgc ttc agc gtg gtg cgg caa tgc tgg gag aag	4098
gcc agc ggg cgg gcg ctg gcc gcc aag atc atc ccc tac cac ccc aag	4146
gac aag aca gca gtg ctg cgc gaa tac gag gcc ctg aag ggc ctg cgc	4194
cac ccg cac ctg gcc cag ctg cac gca gcc tac ctg agc ccc cgg cac	4242

```

ctg gtg ctc atc ttg gag ctg tgc tct ggg ccc gag ctg ctc ccc tgc 4290
ctg gcc gag agg gcc tcc tac tca gaa tcc gag gtg aag gac tac ctg 4338
tgg cag atg ttg agt gcc acc cag tac ctg cac aac cag cac atc ctg 4386
cac ctg gac ctg agg tcc gag aac atg atc atc acc gaa tac aac ctg 4434
ctc aag gtc gtg gac ctg ggc aat gca cag agc ctc agc cag gag aag 4482
gtg ctg ccc tca gac aag ttc aag gac tac cta gag acc atg gct cca 4530
gag ctc ctg gag ggc cag ggg gct gtt cca cag aca gac atc tgg gcc 4578
atc ggt gtg aca gcc ttc atc atg ctg agc gcc gag tac ccg gtg agc 4626
agc gag ggt gca cgc gac ctg cag aga gga ctg cgc aag ggg ctg gtc 4674
cgg ctg agc cgc tgc tac gcg ggg ctg tcc ggg ggc gcc gtg gcc ttc 4722
ctg cgc agc act ctg tgc gcc cag ccc tgg ggc cgg ccc tgc gcg tcc 4770
agc tgc ctg cag tgc ccg tgg cta aca gag gag ggc ccg gcc tgt tcg 4818
cgg ccc gcg ccc gtg acc ttc cct acc gcg cgg ctg cgc gtc ttc gtg 4866
cgc aat cgc gag aag aga cgc gcg ctg ctg tac aag agg cac aac ctg 4914
gcc cag gtg cgc tgagggtcgc cccggccaca cccttggtct ccccgctggg 4966
ggtcgctgca gacgcgccaa taaaaacgca cagccgggcg a 5007

```

<210> 4

<211> 1610

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Gln Val Thr Ile Glu Asp Val Gln Ala Gln Thr Gly Gly Thr Ala
 1           5           10           15
Gln Phe Glu Ala Ile Ile Glu Gly Asp Pro Gln Pro Ser Val Thr Trp
      20           25           30
Tyr Lys Asp Ser Val Gln Leu Val Asp Ser Thr Arg Leu Ser Gln Gln
      35           40           45
Gln Glu Gly Thr Thr Tyr Ser Leu Val Leu Arg His Val Ala Ser Lys
      50           55           60
Asp Ala Gly Val Tyr Thr Cys Leu Ala Gln Asn Thr Gly Gly Gln Val
      65           70           75           80
Leu Cys Lys Ala Glu Leu Leu Val Leu Gly Gly Asp Asn Glu Pro Asp
      85           90           95
Ser Glu Lys Gln Ser His Arg Arg Lys Leu His Ser Phe Tyr Glu Val
      100          105          110
Lys Glu Glu Ile Gly Arg Gly Val Phe Gly Phe Val Lys Arg Val Gln
      115          120          125
His Lys Gly Asn Lys Ile Leu Cys Ala Ala Lys Phe Ile Pro Leu Arg
      130          135          140
Ser Arg Thr Arg Ala Gln Ala Tyr Arg Glu Arg Asp Ile Leu Ala Ala
      145          150          155          160
Leu Ser His Pro Leu Val Thr Gly Leu Leu Asp Gln Phe Glu Thr Arg
      165          170          175
Lys Thr Leu Ile Leu Ile Leu Glu Leu Cys Ser Ser Glu Glu Leu Leu
      180          185          190
Asp Arg Leu Tyr Arg Lys Gly Val Val Thr Glu Ala Glu Val Lys Val
      195          200          205
Tyr Ile Gln Gln Leu Val Glu Gly Leu His Tyr Leu His Ser His Gly
      210          215          220
Val Leu His Leu Asp Ile Lys Pro Ser Asn Ile Leu Met Val His Pro

```


225					230					235				240
Ala	Arg	Glu	Asp	Ile	Lys	Ile	Cys	Asp	Phe	Gly	Phe	Ala	Gln	Asn Ile
				245					250				255	
Thr	Pro	Ala	Glu	Leu	Gln	Phe	Ser	Gln	Tyr	Gly	Ser	Pro	Glu	Phe Val
			260					265					270	
Ser	Pro	Glu	Ile	Ile	Gln	Gln	Asn	Pro	Val	Ser	Glu	Ala	Ser	Asp Ile
		275					280				285			
Trp	Ala	Met	Gly	Val	Ile	Ser	Tyr	Leu	Ser	Leu	Thr	Cys	Ser	Ser Pro
	290					295					300			
Phe	Ala	Gly	Glu	Ser	Asp	Arg	Ala	Thr	Leu	Leu	Asn	Val	Leu	Glu Gly
305					310					315				320
Arg	Val	Ser	Trp	Ser	Ser	Pro	Met	Ala	Ala	His	Leu	Ser	Glu	Asp Ala
				325					330					335
Lys	Asp	Phe	Ile	Lys	Ala	Thr	Leu	Gln	Arg	Ala	Pro	Gln	Ala	Arg Pro
			340					345					350	
Ser	Ala	Ala	Gln	Cys	Leu	Ser	His	Pro	Trp	Phe	Leu	Lys	Ser	Met Pro
		355					360					365		
Ala	Glu	Glu	Ala	His	Phe	Ile	Asn	Thr	Lys	Gln	Leu	Lys	Phe	Leu Leu
	370					375					380			
Ala	Arg	Ser	Arg	Trp	Gln	Arg	Ser	Leu	Met	Ser	Tyr	Lys	Ser	Ile Leu
385					390					395				400
Val	Met	Arg	Ser	Ile	Pro	Glu	Leu	Leu	Arg	Gly	Pro	Pro	Asp	Ser Pro
				405					410					415
Ser	Leu	Gly	Val	Ala	Arg	His	Leu	Cys	Arg	Asp	Thr	Gly	Gly	Ser Ser
			420					425					430	
Ser	Ser	Ser	Ser	Ser	Ser	Asp	Asn	Glu	Leu	Ala	Pro	Phe	Ala	Arg Ala
		435					440					445		
Lys	Ser	Leu	Pro	Pro	Ser	Pro	Val	Thr	His	Ser	Pro	Leu	Leu	His Pro
	450					455					460			
Arg	Gly	Phe	Leu	Arg	Pro	Ser	Ala	Ser	Leu	Pro	Glu	Glu	Ala	Glu Ala
465					470					475				480
Ser	Glu	Arg	Ser	Thr	Glu	Ala	Pro	Ala	Pro	Pro	Ala	Ser	Pro	Glu Gly
				485					490					495
Ala	Gly	Pro	Pro	Ala	Ala	Gln	Gly	Cys	Val	Pro	Arg	His	Ser	Val Ile
		500						505					510	
Arg	Ser	Leu	Phe	Tyr	His	Gln	Ala	Gly	Glu	Ser	Pro	Glu	His	Gly Ala
	515					520						525		
Leu	Ala	Pro	Gly	Ser	Arg	Arg	His	Pro	Ala	Arg	Arg	His	Leu	Leu
	530					535					540			
Lys	Gly	Gly	Tyr	Ile	Ala	Gly	Ala	Leu	Pro	Gly	Leu	Arg	Glu	Pro Leu
545					550					555				560
Met	Glu	His	Arg	Val	Leu	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Glu	Gln Ala
				565					570					575
Thr	Leu	Leu	Ala	Lys	Ala	Pro	Ser	Phe	Glu	Thr	Ala	Leu	Arg	Leu Pro
			580					585					590	
Ala	Ser	Gly	Thr	His	Leu	Ala	Pro	Gly	His	Ser	His	Ser	Leu	Glu His
		595					600					605		
Asp	Ser	Pro	Ser	Thr	Pro	Arg	Pro	Ser	Ser	Glu	Ala	Cys	Gly	Glu Ala
	610					615					620			
Gln	Arg	Leu	Pro	Ser	Ala	Pro	Ser	Gly	Gly	Ala	Pro	Ile	Arg	Asp Met
625					630					635				640
Gly	His	Pro	Gln	Gly	Ser	Lys	Gln	Leu	Pro	Ser	Thr	Gly	Gly	His Pro
				645					650					655
Gly	Thr	Ala	Gln	Pro	Glu	Arg	Pro	Ser	Pro	Asp	Ser	Pro	Trp	Gly Gln
		660					665					670		
Pro	Ala	Pro	Phe	Cys	His	Pro	Lys	Gln	Gly	Ser	Ala	Pro	Gln	Glu Gly
		675					680					685		

Cys Ser Pro His Pro Ala Val Ala Pro Cys Pro Pro Gly Ser Phe Pro
 690 695 700
 Pro Gly Ser Cys Lys Glu Ala Pro Leu Val Pro Ser Ser Pro Phe Leu
 705 710 715 720
 Gly Gln Pro Gln Ala Pro Pro Ala Pro Ala Lys Ala Ser Pro Pro Leu
 725 730 735
 Asp Ser Lys Met Gly Pro Gly Asp Ile Ser Leu Pro Gly Arg Pro Lys
 740 745 750
 Pro Gly Pro Cys Ser Ser Pro Gly Ser Ala Ser Gln Ala Ser Ser Ser
 755 760 765
 Gln Val Ser Ser Leu Arg Val Gly Ser Ser Gln Val Gly Thr Glu Pro
 770 775 780
 Gly Pro Ser Leu Asp Ala Glu Gly Trp Thr Gln Glu Ala Glu Asp Leu
 785 790 795 800
 Ser Asp Ser Thr Pro Thr Leu Gln Arg Pro Gln Glu Gln Ala Thr Met
 805 810 815
 Arg Lys Phe Ser Leu Gly Gly Arg Gly Gly Tyr Ala Gly Val Ala Gly
 820 825 830
 Tyr Gly Thr Phe Ala Phe Gly Gly Asp Ala Gly Gly Met Leu Gly Gln
 835 840 845
 Gly Pro Met Trp Ala Arg Ile Ala Trp Ala Val Ser Gln Ser Glu Glu
 850 855 860
 Glu Glu Gln Glu Glu Ala Arg Ala Glu Ser Gln Ser Glu Glu Gln Gln
 865 870 875 880
 Glu Ala Arg Ala Glu Ser Pro Leu Pro Gln Val Ser Ala Arg Pro Val
 885 890 895
 Pro Glu Val Gly Arg Ala Pro Thr Arg Ser Ser Pro Glu Pro Thr Pro
 900 905 910
 Trp Glu Asp Ile Gly Gln Val Ser Leu Val Gln Ile Arg Asp Leu Ser
 915 920 925
 Gly Asp Ala Glu Ala Ala Asp Thr Ile Ser Leu Asp Ile Ser Glu Val
 930 935 940
 Asp Pro Ala Tyr Leu Asn Leu Ser Asp Leu Tyr Asp Ile Lys Tyr Leu
 945 950 955 960
 Pro Phe Glu Phe Met Ile Phe Arg Lys Val Pro Lys Ser Ala Gln Pro
 965 970 975
 Glu Pro Pro Ser Pro Met Ala Glu Glu Glu Leu Ala Glu Phe Pro Glu
 980 985 990
 Pro Thr Trp Pro Trp Pro Gly Glu Leu Gly Pro His Ala Gly Leu Glu
 995 1000 1005
 Ile Thr Glu Glu Ser Glu Asp Val Asp Ala Leu Leu Ala Glu Ala Ala
 1010 1015 1020
 Val Gly Arg Lys Arg Lys Trp Ser Ser Pro Ser Arg Ser Leu Phe His
 1025 1030 1035 1040
 Phe Pro Gly Arg His Leu Pro Leu Asp Glu Pro Ala Glu Leu Gly Leu
 1045 1050 1055
 Arg Glu Arg Val Lys Ala Ser Val Glu His Ile Ser Arg Ile Leu Lys
 1060 1065 1070
 Gly Arg Pro Glu Gly Leu Glu Lys Glu Gly Pro Pro Arg Lys Lys Pro
 1075 1080 1085
 Gly Leu Ala Ser Phe Arg Leu Ser Gly Leu Lys Ser Trp Asp Arg Ala
 1090 1095 1100
 Pro Thr Phe Leu Arg Glu Leu Ser Asp Glu Thr Val Val Leu Gly Gln
 1105 1110 1115 1120
 Ser Val Thr Leu Ala Cys Gln Val Ser Ala Gln Pro Ala Ala Gln Ala
 1125 1130 1135
 Thr Trp Ser Lys Asp Gly Ala Pro Leu Glu Ser Ser Ser Arg Val Leu

	1140		1145		1150
Ile Ser Ala Thr Leu Lys Asn Phe Gln Leu Leu Thr Ile Leu Val Val					
	1155		1160		1165
Val Ala Glu Asp Leu Gly Val Tyr Thr Cys Ser Val Ser Asn Ala Leu					
	1170		1175		1180
Gly Thr Val Thr Thr Thr Gly Val Leu Arg Lys Ala Glu Arg Pro Ser					
1185		1190		1195	1200
Ser Ser Pro Cys Pro Asp Ile Gly Glu Val Tyr Ala Asp Gly Val Leu					
	1205		1210		1215
Leu Val Trp Lys Pro Val Glu Ser Tyr Gly Pro Val Thr Tyr Ile Val					
	1220		1225		1230
Gln Cys Ser Leu Glu Gly Gly Ser Trp Thr Thr Leu Ala Ser Asp Ile					
	1235		1240		1245
Phe Asp Cys Cys Tyr Leu Thr Ser Lys Leu Ser Arg Gly Gly Thr Tyr					
	1250		1255		1260
Thr Phe Arg Thr Ala Cys Val Ser Lys Ala Gly Met Gly Pro Tyr Ser					
1265		1270		1275	1280
Ser Pro Ser Glu Gln Val Leu Leu Gly Ala Pro Ser His Leu Ala Ser					
	1285		1290		1295
Glu Glu Glu Ser Gln Gly Arg Ser Ala Gln Pro Leu Pro Ser Thr Lys					
	1300		1305		1310
Thr Phe Ala Phe Gln Thr Gln Ile Gln Arg Gly Arg Phe Ser Val Val					
	1315		1320		1325
Arg Gln Cys Trp Glu Lys Ala Ser Gly Arg Ala Leu Ala Ala Lys Ile					
	1330		1335		1340
Ile Pro Tyr His Pro Lys Asp Lys Thr Ala Val Leu Arg Glu Tyr Glu					
1345		1350		1355	1360
Ala Leu Lys Gly Leu Arg His Pro His Leu Ala Gln Leu His Ala Ala					
	1365		1370		1375
Tyr Leu Ser Pro Arg His Leu Val Leu Ile Leu Glu Leu Cys Ser Gly					
	1380		1385		1390
Pro Glu Leu Leu Pro Cys Leu Ala Glu Arg Ala Ser Tyr Ser Glu Ser					
	1395		1400		1405
Glu Val Lys Asp Tyr Leu Trp Gln Met Leu Ser Ala Thr Gln Tyr Leu					
	1410		1415		1420
His Asn Gln His Ile Leu His Leu Asp Leu Arg Ser Glu Asn Met Ile					
1425		1430		1435	1440
Ile Thr Glu Tyr Asn Leu Leu Lys Val Val Asp Leu Gly Asn Ala Gln					
	1445		1450		1455
Ser Leu Ser Gln Glu Lys Val Leu Pro Ser Asp Lys Phe Lys Asp Tyr					
	1460		1465		1470
Leu Glu Thr Met Ala Pro Glu Leu Leu Glu Gly Gln Gly Ala Val Pro					
	1475		1480		1485
Gln Thr Asp Ile Trp Ala Ile Gly Val Thr Ala Phe Ile Met Leu Ser					
	1490		1495		1500
Ala Glu Tyr Pro Val Ser Ser Glu Gly Ala Arg Asp Leu Gln Arg Gly					
1505		1510		1515	1520
Leu Arg Lys Gly Leu Val Arg Leu Ser Arg Cys Tyr Ala Gly Leu Ser					
	1525		1530		1535
Gly Gly Ala Val Ala Phe Leu Arg Ser Thr Leu Cys Ala Gln Pro Trp					
	1540		1545		1550
Gly Arg Pro Cys Ala Ser Ser Cys Leu Gln Cys Pro Trp Leu Thr Glu					
	1555		1560		1565
Glu Gly Pro Ala Cys Ser Arg Pro Ala Pro Val Thr Phe Pro Thr Ala					
	1570		1575		1580
Arg Leu Arg Val Phe Val Arg Asn Arg Glu Lys Arg Arg Ala Leu Leu					
1585		1590		1595	1600

Tyr Lys Arg His Asn Leu Ala Gln Val Arg
 1605 1610

<210> 5
 <211> 7928
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)...(7847)

<400> 5
 gaattcggcg cgccagatat cacacgtgcc aaggggctgg ctcaactggtg cgcggccga 59
 atg ctg gag agg ttc acc ccc aag aaa gtg aag aaa ggc tcc agc atc 107
 acc ttc tct gtg aag gta gaa gga cgc ccg gtg ccc acc gtg cac tgg 155
 ctc agg gag gag gct gag aga ggc gtg ctg tgg att ggc cct gac aca 203
 ccg ggc tac acc gtg gcc agc tct gcg cag cag cac agc ctg gtc ctg 251
 ctg gac gtg ggc cgg cag cac cag ggc acc tac aca tgc att gcc agc 299
 aac gct gcc ggc cag gcc ctc tgc tcc gcc agc ctg cac gtc tcg ggc 347
 ctg cct aag gtg gag gag cag gag aaa gtg aag gaa gcg ctg att tcc 395
 act ttc ctg cag ggg acc aca caa gcc atc tca gca cag ggg ttg gaa 443
 act gcg agt ttt gct gac ctt ggt ggg cag agg aaa gaa gag cct ctg 491
 gct gcc aag gag gcc ctc ggc cac ctg tcc ctc gct gag gtg ggc aca 539
 gag gag ttc ctg cag aaa ctg acc tcc cag atc act gag atg gta tcg 587
 gcc aag atc acg cag gcc aag ctg cag gtg cca gga ggt gac agt gat 635
 gag gac tcc aag aca cca tct gca tcc ccc cgc cat ggc cga tca cgg 683
 cca tcc tcc agc atc cag gag tct tcc tca gag tca gag gac ggc gat 731
 gcc cga ggc gag atc ttt gac atc tac gtg gtc acc gct gac tac ctg 779
 ccc cta ggg gct gag cag gat gcc atc acg ctg cgg gaa ggc cag tat 827
 gtg gag gtc ctg gat gca gcc cac cca ctg cgc tgg ctt gtc cgc acc 875
 aag ccc acc aag tcc agc ccc tca cgg cag ggc tgg gtg tca cca gcc 923
 tac ctg gac agg agg ctc aag ctg tca cct gag tgg ggg gcc gct gag 971
 gcc cct gag ttc cct ggg gag gct gtg tct gaa gac gaa tac aag gca 1019
 agg ctg agc tct gtg atc cag gag ctg ctg agt tct gag cag gcc ttc 1067
 gtg gag gag ctg cag ttc ctg cag agc cac cac ctg cag cac ctg gag 1115
 cgc tgc ccc cac gtg ccc ata gcc gtg gcc ggc cag aag gca gtc atc 1163
 ttc cgc aat gtg cgg gac atc ggc cgc ttc cac agc agc ttc ctg cag 1211
 gag ttg cag cag tgc gac acg gac gac gac gtg gcc atg tgc ttc atc 1259
 aag aac cag gcg gcc ttt gag cag tac ctg gag ttc ctg gtg ggg cgt 1307
 gtg cag gct gag tcg gtg gtc gtc agc acg gcc atc cag gag ttc tac 1355
 aag aaa tac gcg gag gag gcc ctg ttg gca ggg gac ccc tct cag ccc 1403
 ccg cca cca cct ctg cag cac tac ctg gag cag cca gtg gag cgg gtg 1451
 cag cgc tac cag gcc ttg ctg aag gag ttg atc cgc aac aag gcg cgg 1499
 aac aga cca aac tgc gcg ctg ctg gag cag gcc tat gcc gtg gtg tct 1547
 gcc ctg cca cag cgc gct gag aac aag ctg cac gtg tcc ctc atg gag 1595
 aac tac cca ggc acc ctg gag gcc ctg ggc gag ccc atc cgc cag ggc 1643
 cac ttc atc gtg tgg gag ggt gca ccg ggg gcc cgc atg ccc tgg aag 1691
 ggc cac aac cgt cac gtg ttc ctc ttc cgc aac cac ctg gta atc tgc 1739

aag ccc cgg cga gac tcc cgc acc gat acc gtc agc tac gtg ttc cgg	1787
aac atg atg aag ctg agc agc atc gac ctg aac gac cag gtg gag ggg	1835
gat gac cgc gcc ttc gag gtg tgg cag gag cgg gag gac tcg gtg cgc	1883
aag tac ctg ctg cag gca cgg aca gcc att atc aag agc tcg tgg gtg	1931
aag gag atc tgt ggc atc cag cag cgt ctg gcc ctg cct gtg tgg cgg	1979
ccc ccg gac ttt gaa gag gag ctg gcc gac tgc aca gcc gag ctg ggt	2027
gag aca gtc aag ctg gcc tgc cgc gtg acg ggc aca ccc aag cct gtc	2075
atc agc tgg tac aaa gat ggg aaa gca gtg cag gtg gac ccc cac cac	2123
atc ctc att gaa gac cct gat ggc tgc tgt gca ctc atc ctg gac agc	2171
ctg acc ggt gtg gac tct ggc cag tac atg tgc ttc gcg gcc agc gcc	2219
gct ggc aac tgc agt acc ctg ggc aag atc ctg gtg caa gtc cca cca	2267
cgg ttc gtg aac aag gtc cgg gcc tca ccc ttt gtg gag gga gag gac	2315
gcc cag ttc acc tgc acc atc gaa ggc gcc ccg tac ccg cag atc agg	2363
tgg tac aag gac ggg gcc ctg ctg acc act ggc aac aag ttc cag aca	2411
ctg agt gag cct gcg agc ggc ctg cta gtg ctg gtg atc cgg gcg gcc	2459
agc aag gag gac ctg ggg ctc tac gag tgt gag ctg gtg aac cgg ctg	2507
ggc tcc gcg cgg gct agt gcg gag ctg cgc att cag agc ccc atg ctg	2555
cag gcc cag gag cag tgt cac agg gag cag ctc gtg gct gca gtg gaa	2603
gac acc acc ctg gag cga gcg gac cag gag gtc aca tct gtc ctg aag	2651
aga ctg ctg ggc ccc aag gcg cca ggc ccc tcc aca ggg gac ctc act	2699
ggc cct ggc ccc tgc ccc agg ggg gca ccc gca ctc cag gaa acc ggc	2747
tcc cag ccc cca gtc acc gga act tgc gag gca cct gcc gtg ccc ccg	2795
agg gtg cca cag ccc ctc ctc cac gaa ggc cca gag cag gag ccg gag	2843
gcc att gcc aga gcc cag gaa tgg act gtg ccc att cgg atg gag ggt	2891
gca gcc tgg ccc ggg gca ggc aca ggg gag ctg ctc tgg gac gtc cac	2939
agc cac gtg gtc aga gag acc aca cag agg acc tac aca tac cag gcc	2987
atc gac acg cac acc gca cgg ccc cca tcc atg cag gta acc atc gag	3035
gat gtg cag gca cag aca ggc gga acg gcc caa ttc gag gct atc att	3083
gag ggc gac cca cag ccc tgc gtg acc tgg tac aag gac agc gtc cag	3131
ctg gtg gac agc acc cgg ctt agc cag cag caa gaa ggc acc aca tac	3179
tcc ctg gtg ctg agg cat gtg gcc tgc aag gat gcc ggc gtt tac acc	3227
tgc ctg gcc caa aac act ggt ggc cag gtg ctc tgc aag gca gag ctg	3275
ctg gtg ctt ggg ggg gac aat gag ccg gac tca gag aag caa agc cac	3323
cgg agc aag ctg cac tcc ttc tat gat ggc gtc aag gag gag att gga agg	3371
ggc gtg ttt ggc ttc gta aaa aga gtg cag cac aaa gga aac aag atc	3419
ttg tgc gct gcc aag ttc atc ccc cta cgg agc aga act cgg gcc cag	3467
gca tac agg gag cga gac atc ctg gcc gcg ctg agc cac ccg ctg gtc	3515
acg ggg ctg ctg gac cag ttt gag acc cgc aag acc ctc atc ctc atc	3563
ctg gag ctg tgc tca tcc gag gag ctg ctg gac cgc ctg tac agg aag	3611
ggc gtg gtg acg gag gcc gag gtc aag gtc tac atc cag cag ctg gtg	3659
gag ggg ctg cac tac ctg cac agc cat ggc gtt ctc cac ctg gac ata	3707
aag ccc tct aac atc ctg atg gtg cat cct gcc cgg gaa gac att aaa	3755
atc tgc gac ttt ggc ttt gcc cag aac atc acc cca gca gag ctg cag	3803
ttc agc cag tac ggc tcc cct gag ttc gtc tcc ccc gag atc atc cag	3851
cag aac cct gtg agc gaa gcc tcc gac att tgg gcc atg ggt gtc atc	3899
tcc tac ctc agc ctg acc tgc tca tcc cca ttt gcc ggc gag agt gac	3947
cgt gcc acc ctc ctg aac gtc ctg gag ggg cgc gtg tca tgg agc agc	3995
ccc atg gct gcc cac ctc agc gaa gac gcc aaa gac ttc atc aag gct	4043
acg ctg cag aga gcc cct cag gcc cgg cct agt gcg gcc cag tgc ctc	4091
tcc cac ccc tgg ttc ctg aaa tcc atg cct gcg gag gag gcc cac ttc	4139
atc aac acc aag cag ctc aag ttc ctc ctg gcc cga agt cgc tgg cag	4187
cgt tcc ctg atg agc tac aag tcc atc ctg gtg atg cgc tcc atc cct	4235
gag ctg ctg cgg ggc cca ccc gac agc ccc tcc ctc ggc gta gcc cgg	4283
cac ctc tgc agg gac act ggt ggc tcc tcc agt tcc tcc tcc tcc tct	4331
gac aac gag ctc gcc cca ttt gcc cgg gct aag tca ctg cca ccc tcc	4379
ccg gtg aca cac tca cca ctg ctg cac ccc cgg ggc ttc ctg cgg ccc	4427
tgc gcc agc ctg cct gag gaa gcc gag gcc agt gag cgc tcc acc gag	4475

gcc cca gct ccg cct gca tct ccc gag ggt gcc ggg cca ccg gcc gcc	4523
cag ggc tgc gtg ccc cgg cac agc gtc atc cgc agc ctg ttc tac cac	4571
cag gcg ggt gag agc cct gag cac ggg gcc ctg gcc ccg ggg agc agg	4619
cgg cac ccg gcc cgg cgg cgg cac ctg ctg aag ggc ggg tac att gcg	4667
ggg gcg ctg cca ggc ctg cgc gag cca ctg atg gag cac cgc gtg ctg	4715
gag gag gag gcc gcc agg gag gag cag gcc acc ctc ctg gcc aaa gcc	4763
ccc tca ttc gag act gcc ctc cgg ctg cct gcc tct ggc acc cac ttg	4811
gcc cct ggc cac agc cac tcc ctg gaa cat gac tct ccg agc acc ccc	4859
cgc ccc tcc tcg gag gcc tgc ggt gag gca cag cga ctg cct tca gcc	4907
ccc tcc ggg ggg gcc cct atc agg gac atg ggg cac cct cag ggc tcc	4955
aag cag ctt cca tcc act ggt ggc cac cca ggc act gct cag cca gag	5003
agg cca tcc ccg gac agc cct tgg ggg cag cca gcc cct ttc tgc cac	5051
ccc aag cag ggt tct gcc ccc cag gag ggc tgc agc ccc cac gca	5099
gtt gcc cca tgc cct cct ggc tcc ttc cct cca gga tct tgc aaa gag	5147
gcc ccc tta gta ccc tca agc ccc ttc ttg gga cag ccc cag gca ccc	5195
cct gcc cct gcc aaa gca agc ccc cca ttg gac tct aag atg ggg cct	5243
gga gac atc tct ctt cct ggg agg cca aaa ccc ggc ccc tgc agt tcc	5291
cca ggg tca gcc tcc cag gcg agc tct tcc caa gtg agc tcc ctc agg	5339
gtg ggc tcc tcc cag gtg ggc aca gag cct ggc ccc tcc ctg gat gcg	5387
gag ggc tgg acc cag gag gct gag gat ctg tcc gac tcc aca ccc acc	5435
ttg cag ccg cct cag gaa cag gcg acc atg cgc aag ttc tcc ctg ggt	5483
ggt cgc ggg ggc tac gca ggc gtg gct ggc tat ggc acc ttt gcc ttt	5531
ggt gga gat gca ggg ggc atg ctg ggg cag ggg ccc atg tgg gcc agg	5579
ata gcc tgg gct gtg tcc cag tca gag gag gag gag cag gag gag gcc	5627
agg gct gag tcc cag tcg gag gag cag cag gag gcc agg gct gag agc	5675
cca ctg ccc cag gtc agt gca agg cct gtg cct gag gtc ggc agg gct	5723
ccc acc agg agc tct cca gag ccc acc cca tgg gag gac atc ggg cag	5771
gtc tcc ctg gtg cag atc cgg gac ctg tca ggt gat gcg gag gcg gcc	5819
gac aca ata tcc ctg gac att tcc gag gtg gac ccc gcc tac ctc aac	5867
ctc tca gac ctg tac gat atc aag tac ctc cca ttc gag ttt atg atc	5915
ttc agg aaa gtc ccc aag tcc gct cag cca gag ccg ccc tcc ccc atg	5963
gct gag gag gag ctg gcc gag ttc ccg gag ccc acg tgg ccc tgg cca	6011
ggt gaa ctg ggc ccc cac gca ggc ctg gag atc aca gag gag tca gag	6059
gat gtg gac gcg ctg ctg gca gag gct gcc gtg ggc agg aag cgc aag	6107
tgg tcc tcg ccg tca cgc agc ctc ttc cac ttc cct ggg agg cac ctg	6155
ccg ctg gat gag cct gca gag ctg ggg ctg cgt gag aga gtg aag gcc	6203
tcc gtg gag cac atc tcc ccg atc ctg aag ggc agg ccg gaa ggt ctg	6251
gag aag gag ggg ccc ccc agg aag aag cca ggc ctt gct tcc ttc cgg	6299
ctc tca ggt ctg aag agc tgg gac cga gcg ccg aca ttc cta agg gag	6347
ctc tca gat gag act gtg gtc ctg ggc cag tca gtg aca ctg gcc tgc	6395
cag gtg tca gcc cag cca gct gcc cag gcc acc tgg agc aaa gac gga	6443
gcc ccc ctg gag agc agc agc cgt gtc ctc atc tct gcc acc ctc aag	6491
aac ttc cag ctt ctg acc atc ctg gtg gtg gtg gct gag gac ctg ggt	6539
gtg tac acc tgc agc gtg agc aat gcg ctg ggg aca gtg acc acc acg	6587
ggc gtc ctc ccg aag gca gag cgc ccc tca tct tcg cca tgc ccg gat	6635
atc ggg gag gtg tac gcg gat ggg gtg ctg gtc tgg aag ccc gtg	6683
gaa tcc tac ggc cct gtg acc tac att gtg cag tgc agc cta gaa ggc	6731
ggc agc tgg acc aca ctg gcc tcc gac atc ttt gac tgc tgc tac ctg	6779
acc agc aag ctc tcc ccg ggt ggc acc tac acc ttc cgc acg gca tgt	6827
gtc agc aag gca gga atg ggt ccc tac agc agc ccc tcg gag caa gtc	6875
ctc ctg gga gcg ccc agc cac ctg gcc tct gag gag gag agc cag ggg	6923
cgg tca gcc caa ccc ctg ccc agc aca aag acc ttc gca ttc cag aca	6971
cag atc cag agg ggc cgc ttc agc gtg gtg cgg caa tgc tgg gag aag	7019
gcc agc ggg ccg gcg ctg gcc gcc aag atc atc ccc tac cac ccc aag	7067
gac aag aca gca gtg ctg cgc gaa tac gag gcc ctc aag ggc ctg cgc	7115
cac ccg cac ctg gcc cag ctg cac gca gcc tac ctc agc ccc ccg cac	7163
ctg gtg ctc atc ttg gag ctg tgc tct ggg ccc gag ctg ctc ccc tgc	7211

```

ctg gcc gag agg gcc tcc tac tca gaa tcc gag gtg aag gac tac ctg 7259
tgg cag atg ttg agt gcc acc cag tac ctg cac aac cag cac atc ctg 7307
cac ctg gac ctg agg tcc gag aac atg atc atc acc gaa tac aac ctg 7355
ctc aag gtc gtg gac ctg ggc aat gca cag agc ctc agc cag gag aag 7403
gtg ctg ccc tca gac aag ttc aag gac tac cta gag acc atg gct cca 7451
gag ctc ctg gag ggc cag ggg gct gtt cca cag aca gac atc tgg gcc 7499
atc ggt gtg aca gcc ttc atc atg ctg agc gcc gag tac ccg gtg agc 7547
agc gag ggt gca cgc gac ctg cag aga gga ctg cgc aag ggg ctg gtc 7595
cgg ctg agc cgc tgc tac gcg ggg ctg tcc ggg ggc gcc gtg gcc ttc 7643
ctg cgc agc act ctg tgc gcc cag ccc tgg ggc cgg ccc tgc gcg tcc 7691
agc tgc ctg cag tgc ccg tgg cta aca gag gag ggc ccg gcc tgt tgc 7739
cgg ccc gcg ccc gtg acc ttc cct acc gcg cgg ctg cgc gtc ttc gtg 7787
cgc aat cgc gag aag aga cgc gcg ctg ctg tac aag agg cac aac ctg 7835
gcc cag gtg cgc tgagggtcgcc ccggccacac ccttggtctc cccgctgggg 7888
gtcgtgtgacg acgcgccaat aaaaacgcac agccgggcga 7928

```

<210> 6

<211> 2596

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Leu Glu Arg Phe Thr Pro Lys Lys Val Lys Lys Gly Ser Ser Ile
 1          5          10          15
Thr Phe Ser Val Lys Val Glu Gly Arg Pro Val Pro Thr Val His Trp
 20          25          30
Leu Arg Glu Glu Ala Glu Arg Gly Val Leu Trp Ile Gly Pro Asp Thr
 35          40          45
Pro Gly Tyr Thr Val Ala Ser Ser Ala Gln Gln His Ser Leu Val Leu
 50          55          60
Leu Asp Val Gly Arg Gln His Gln Gly Thr Tyr Thr Cys Ile Ala Ser
 65          70          75          80
Asn Ala Ala Gly Gln Ala Leu Cys Ser Ala Ser Leu His Val Ser Gly
 85          90          95
Leu Pro Lys Val Glu Glu Gln Glu Lys Val Lys Glu Ala Leu Ile Ser
100          105          110
Thr Phe Leu Gln Gly Thr Thr Gln Ala Ile Ser Ala Gln Gly Leu Glu
115          120          125
Thr Ala Ser Phe Ala Asp Leu Gly Gly Gln Arg Lys Glu Glu Pro Leu
130          135          140
Ala Ala Lys Glu Ala Leu Gly His Leu Ser Leu Ala Glu Val Gly Thr
145          150          155          160
Glu Glu Phe Leu Gln Lys Leu Thr Ser Gln Ile Thr Glu Met Val Ser
165          170          175
Ala Lys Ile Thr Gln Ala Lys Leu Gln Val Pro Gly Gly Asp Ser Asp
180          185          190
Glu Asp Ser Lys Thr Pro Ser Ala Ser Pro Arg His Gly Arg Ser Arg
195          200          205
Pro Ser Ser Ser Ile Gln Glu Ser Ser Ser Glu Ser Glu Asp Gly Asp
210          215          220
Ala Arg Gly Glu Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu
225          230          235          240

```

Pro Leu Gly Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr
 245 250 255
 Val Glu Val Leu Asp Ala Ala His Pro Leu Arg Trp Leu Val Arg Thr
 260 265 270
 Lys Pro Thr Lys Ser Ser Pro Ser Arg Gln Gly Trp Val Ser Pro Ala
 275 280 285
 Tyr Leu Asp Arg Arg Leu Lys Leu Ser Pro Glu Trp Gly Ala Ala Glu
 290 295 300
 Ala Pro Glu Phe Pro Gly Glu Ala Val Ser Glu Asp Glu Tyr Lys Ala
 305 310 315 320
 Arg Leu Ser Ser Val Ile Gln Glu Leu Leu Ser Ser Glu Gln Ala Phe
 325 330 335
 Val Glu Glu Leu Gln Phe Leu Gln Ser His His Leu Gln His Leu Glu
 340 345 350
 Arg Cys Pro His Val Pro Ile Ala Val Ala Gly Gln Lys Ala Val Ile
 355 360 365
 Phe Arg Asn Val Arg Asp Ile Gly Arg Phe His Ser Ser Phe Leu Gln
 370 375 380
 Glu Leu Gln Gln Cys Asp Thr Asp Asp Val Ala Met Cys Phe Ile
 385 390 395 400
 Lys Asn Gln Ala Ala Phe Glu Gln Tyr Leu Glu Phe Leu Val Gly Arg
 405 410 415
 Val Gln Ala Glu Ser Val Val Val Ser Thr Ala Ile Gln Glu Phe Tyr
 420 425 430
 Lys Lys Tyr Ala Glu Glu Ala Leu Leu Ala Gly Asp Pro Ser Gln Pro
 435 440 445
 Pro Pro Pro Pro Leu Gln His Tyr Leu Glu Gln Pro Val Glu Arg Val
 450 455 460
 Gln Arg Tyr Gln Ala Leu Leu Lys Glu Leu Ile Arg Asn Lys Ala Arg
 465 470 475 480
 Asn Arg Gln Asn Cys Ala Leu Leu Glu Gln Ala Tyr Ala Val Val Ser
 485 490 495
 Ala Leu Pro Gln Arg Ala Glu Asn Lys Leu His Val Ser Leu Met Glu
 500 505 510
 Asn Tyr Pro Gly Thr Leu Glu Ala Leu Gly Glu Pro Ile Arg Gln Gly
 515 520 525
 His Phe Ile Val Trp Glu Gly Ala Pro Gly Ala Arg Met Pro Trp Lys
 530 535 540
 Gly His Asn Arg His Val Phe Leu Phe Arg Asn His Leu Val Ile Cys
 545 550 555 560
 Lys Pro Arg Arg Asp Ser Arg Thr Asp Thr Val Ser Tyr Val Phe Arg
 565 570 575
 Asn Met Met Lys Leu Ser Ser Ile Asp Leu Asn Asp Gln Val Glu Gly
 580 585 590
 Asp Asp Arg Ala Phe Glu Val Trp Gln Glu Arg Glu Asp Ser Val Arg
 595 600 605
 Lys Tyr Leu Leu Gln Ala Arg Thr Ala Ile Ile Lys Ser Ser Trp Val
 610 615 620
 Lys Glu Ile Cys Gly Ile Gln Gln Arg Leu Ala Leu Pro Val Trp Arg
 625 630 635 640
 Pro Pro Asp Phe Glu Glu Glu Leu Ala Asp Cys Thr Ala Glu Leu Gly
 645 650 655
 Glu Thr Val Lys Leu Ala Cys Arg Val Thr Gly Thr Pro Lys Pro Val
 660 665 670
 Ile Ser Trp Tyr Lys Asp Gly Lys Ala Val Gln Val Asp Pro His His
 675 680 685
 Ile Leu Ile Glu Asp Pro Asp Gly Ser Cys Ala Leu Ile Leu Asp Ser

690	695	700
Leu Thr Gly Val Asp Ser Gly Gln Tyr Met Cys Phe Ala Ala Ser Ala		
705	710	715
Ala Gly Asn Cys Ser Thr Leu Gly Lys Ile Leu Val Gln Val Pro Pro		720
	725	730
Arg Phe Val Asn Lys Val Arg Ala Ser Pro Phe Val Glu Gly Glu Asp		735
	740	745
Ala Gln Phe Thr Cys Thr Ile Glu Gly Ala Pro Tyr Pro Gln Ile Arg		750
	755	760
Trp Tyr Lys Asp Gly Ala Leu Leu Thr Thr Gly Asn Lys Phe Gln Thr		765
	770	775
Leu Ser Glu Pro Arg Ser Gly Leu Leu Val Leu Val Ile Arg Ala Ala		780
	785	790
Ser Lys Glu Asp Leu Gly Leu Tyr Glu Cys Glu Leu Val Asn Arg Leu		795
	805	810
Gly Ser Ala Arg Ala Ser Ala Glu Leu Arg Ile Gln Ser Pro Met Leu		815
	820	825
Gln Ala Gln Glu Gln Cys His Arg Glu Gln Leu Val Ala Ala Val Glu		830
	835	840
Asp Thr Thr Leu Glu Arg Ala Asp Gln Glu Val Thr Ser Val Leu Lys		845
	850	855
Arg Leu Leu Gly Pro Lys Ala Pro Gly Pro Ser Thr Gly Asp Leu Thr		860
	865	870
Gly Pro Gly Pro Cys Pro Arg Gly Ala Pro Ala Leu Gln Glu Thr Gly		875
	885	890
Ser Gln Pro Pro Val Thr Gly Thr Ser Glu Ala Pro Ala Val Pro Pro		895
	900	905
Arg Val Pro Gln Pro Leu Leu His Glu Gly Pro Glu Gln Glu Pro Glu		910
	915	920
Ala Ile Ala Arg Ala Gln Glu Trp Thr Val Pro Ile Arg Met Glu Gly		925
	930	935
Ala Ala Trp Pro Gly Ala Gly Thr Gly Glu Leu Leu Trp Asp Val His		940
	945	950
Ser His Val Val Arg Glu Thr Thr Gln Arg Thr Tyr Thr Tyr Gln Ala		955
	965	970
Ile Asp Thr His Thr Ala Arg Pro Pro Ser Met Gln Val Thr Ile Glu		975
	980	985
Asp Val Gln Ala Gln Thr Gly Gly Thr Ala Gln Phe Glu Ala Ile Ile		990
	995	1000
Glu Gly Asp Pro Gln Pro Ser Val Thr Trp Tyr Lys Asp Ser Val Gln		1005
	1010	1015
Leu Val Asp Ser Thr Arg Leu Ser Gln Gln Gln Glu Gly Thr Thr Tyr		1020
	1025	1030
Ser Leu Val Leu Arg His Val Ala Ser Lys Asp Ala Gly Val Tyr Thr		1035
	1045	1050
Cys Leu Ala Gln Asn Thr Gly Gly Gln Val Leu Cys Lys Ala Glu Leu		1055
	1060	1065
Leu Val Leu Gly Gly Asp Asn Glu Pro Asp Ser Glu Lys Gln Ser His		1070
	1075	1080
Arg Arg Lys Leu His Ser Phe Tyr Glu Val Lys Glu Glu Ile Gly Arg		1085
	1090	1095
Gly Val Phe Gly Phe Val Lys Arg Val Gln His Lys Gly Asn Lys Ile		1100
	1105	1110
Leu Cys Ala Ala Lys Phe Ile Pro Leu Arg Ser Arg Thr Arg Ala Gln		1115
	1125	1130
Ala Tyr Arg Glu Arg Asp Ile Leu Ala Ala Leu Ser His Pro Leu Val		1135
	1140	1145
		1150

Thr Gly Leu Leu Asp Gln Phe Glu Thr Arg Lys Thr Leu Ile Leu Ile
 1155 1160 1165
 Leu Glu Leu Cys Ser Ser Glu Glu Leu Leu Asp Arg Leu Tyr Arg Lys
 1170 1175 1180
 Gly Val Val Thr Glu Ala Glu Val Lys Val Tyr Ile Gln Gln Leu Val
 1185 1190 1195 1200
 Glu Gly Leu His Tyr Leu His Ser His Gly Val Leu His Leu Asp Ile
 1205 1210 1215
 Lys Pro Ser Asn Ile Leu Met Val His Pro Ala Arg Glu Asp Ile Lys
 1220 1225 1230
 Ile Cys Asp Phe Gly Phe Ala Gln Asn Ile Thr Pro Ala Glu Leu Gln
 1235 1240 1245
 Phe Ser Gln Tyr Gly Ser Pro Glu Phe Val Ser Pro Glu Ile Ile Gln
 1250 1255 1260
 Gln Asn Pro Val Ser Glu Ala Ser Asp Ile Trp Ala Met Gly Val Ile
 1265 1270 1275 1280
 Ser Tyr Leu Ser Leu Thr Cys Ser Ser Pro Phe Ala Gly Glu Ser Asp
 1285 1290 1295
 Arg Ala Thr Leu Leu Asn Val Leu Glu Gly Arg Val Ser Trp Ser Ser
 1300 1305 1310
 Pro Met Ala Ala His Leu Ser Glu Asp Ala Lys Asp Phe Ile Lys Ala
 1315 1320 1325
 Thr Leu Gln Arg Ala Pro Gln Ala Arg Pro Ser Ala Ala Gln Cys Leu
 1330 1335 1340
 Ser His Pro Trp Phe Leu Lys Ser Met Pro Ala Glu Glu Ala His Phe
 1345 1350 1355 1360
 Ile Asn Thr Lys Gln Leu Lys Phe Leu Leu Ala Arg Ser Arg Trp Gln
 1365 1370 1375
 Arg Ser Leu Met Ser Tyr Lys Ser Ile Leu Val Met Arg Ser Ile Pro
 1380 1385 1390
 Glu Leu Leu Arg Gly Pro Pro Asp Ser Pro Ser Leu Gly Val Ala Arg
 1395 1400 1405
 His Leu Cys Arg Asp Thr Gly Gly Ser Ser Ser Ser Ser Ser Ser
 1410 1415 1420
 Asp Asn Glu Leu Ala Pro Phe Ala Arg Ala Lys Ser Leu Pro Pro Ser
 1425 1430 1435 1440
 Pro Val Thr His Ser Pro Leu Leu His Pro Arg Gly Phe Leu Arg Pro
 1445 1450 1455
 Ser Ala Ser Leu Pro Glu Glu Ala Glu Ala Ser Glu Arg Ser Thr Glu
 1460 1465 1470
 Ala Pro Ala Pro Pro Ala Ser Pro Glu Gly Ala Gly Pro Pro Ala Ala
 1475 1480 1485
 Gln Gly Cys Val Pro Arg His Ser Val Ile Arg Ser Leu Phe Tyr His
 1490 1495 1500
 Gln Ala Gly Glu Ser Pro Glu His Gly Ala Leu Ala Pro Gly Ser Arg
 1505 1510 1515 1520
 Arg His Pro Ala Arg Arg His Leu Leu Lys Gly Gly Tyr Ile Ala
 1525 1530 1535
 Gly Ala Leu Pro Gly Leu Arg Glu Pro Leu Met Glu His Arg Val Leu
 1540 1545 1550
 Glu Glu Glu Ala Ala Arg Glu Glu Gln Ala Thr Leu Leu Ala Lys Ala
 1555 1560 1565
 Pro Ser Phe Glu Thr Ala Leu Arg Leu Pro Ala Ser Gly Thr His Leu
 1570 1575 1580
 Ala Pro Gly His Ser His Ser Leu Glu His Asp Ser Pro Ser Thr Pro
 1585 1590 1595 1600
 Arg Pro Ser Ser Glu Ala Cys Gly Glu Ala Gln Arg Leu Pro Ser Ala

				1605					1610				1615		
Pro	Ser	Gly	Gly	Ala	Pro	Ile	Arg	Asp	Met	Gly	His	Pro	Gln	Gly	Ser
				1620					1625					1630	
Lys	Gln	Leu	Pro	Ser	Thr	Gly	Gly	His	Pro	Gly	Thr	Ala	Gln	Pro	Glu
				1635					1640					1645	
Arg	Pro	Ser	Pro	Asp	Ser	Pro	Trp	Gly	Gln	Pro	Ala	Pro	Phe	Cys	His
				1650					1655					1660	
Pro	Lys	Gln	Gly	Ser	Ala	Pro	Gln	Glu	Gly	Cys	Ser	Pro	His	Pro	Ala
				1665					1670					1675	
Val	Ala	Pro	Cys	Pro	Pro	Gly	Ser	Phe	Pro	Pro	Gly	Ser	Cys	Lys	Glu
				1685					1690					1695	
Ala	Pro	Leu	Val	Pro	Ser	Ser	Pro	Phe	Leu	Gly	Gln	Pro	Gln	Ala	Pro
				1700					1705					1710	
Pro	Ala	Pro	Ala	Lys	Ala	Ser	Pro	Pro	Leu	Asp	Ser	Lys	Met	Gly	Pro
				1715					1720					1725	
Gly	Asp	Ile	Ser	Leu	Pro	Gly	Arg	Pro	Lys	Pro	Gly	Pro	Cys	Ser	Ser
				1730					1735					1740	
Pro	Gly	Ser	Ala	Ser	Gln	Ala	Ser	Ser	Ser	Gln	Val	Ser	Ser	Leu	Arg
				1745					1750					1755	
Val	Gly	Ser	Ser	Gln	Val	Gly	Thr	Glu	Pro	Gly	Pro	Ser	Leu	Asp	Ala
				1765					1770					1775	
Glu	Gly	Trp	Thr	Gln	Glu	Ala	Glu	Asp	Leu	Ser	Asp	Ser	Thr	Pro	Thr
				1780					1785					1790	
Leu	Gln	Arg	Pro	Gln	Glu	Gln	Ala	Thr	Met	Arg	Lys	Phe	Ser	Leu	Gly
				1795					1800					1805	
Gly	Arg	Gly	Gly	Tyr	Ala	Gly	Val	Ala	Gly	Tyr	Gly	Thr	Phe	Ala	Phe
				1810					1815					1820	
Gly	Gly	Asp	Ala	Gly	Gly	Met	Leu	Gly	Gln	Gly	Pro	Met	Trp	Ala	Arg
				1825					1830					1835	
Ile	Ala	Trp	Ala	Val	Ser	Gln	Ser	Glu	Glu	Glu	Glu	Gln	Glu	Glu	Ala
				1845					1850					1855	
Arg	Ala	Glu	Ser	Gln	Ser	Glu	Glu	Gln	Gln	Glu	Ala	Arg	Ala	Glu	Ser
				1860					1865					1870	
Pro	Leu	Pro	Gln	Val	Ser	Ala	Arg	Pro	Val	Pro	Glu	Val	Gly	Arg	Ala
				1875					1880					1885	
Pro	Thr	Arg	Ser	Ser	Pro	Glu	Pro	Thr	Pro	Trp	Glu	Asp	Ile	Gly	Gln
				1890					1895					1900	
Val	Ser	Leu	Val	Gln	Ile	Arg	Asp	Leu	Ser	Gly	Asp	Ala	Glu	Ala	Ala
				1905					1910					1915	
Asp	Thr	Ile	Ser	Leu	Asp	Ile	Ser	Glu	Val	Asp	Pro	Ala	Tyr	Leu	Asn
				1925					1930					1935	
Leu	Ser	Asp	Leu	Tyr	Asp	Ile	Lys	Tyr	Leu	Pro	Phe	Glu	Phe	Met	Ile
				1940					1945					1950	
Phe	Arg	Lys	Val	Pro	Lys	Ser	Ala	Gln	Pro	Glu	Pro	Pro	Ser	Pro	Met
				1955					1960					1965	
Ala	Glu	Glu	Glu	Leu	Ala	Glu	Phe	Pro	Glu	Pro	Thr	Trp	Pro	Trp	Pro
				1970					1975					1980	
Gly	Glu	Leu	Gly	Pro	His	Ala	Gly	Leu	Glu	Ile	Thr	Glu	Glu	Ser	Glu
				1985					1990					1995	
Asp	Val	Asp	Ala	Leu	Leu	Ala	Glu	Ala	Ala	Val	Gly	Arg	Lys	Arg	Lys
				2005					2010					2015	
Trp	Ser	Ser	Pro	Ser	Arg	Ser	Leu	Phe	His	Phe	Pro	Gly	Arg	His	Leu
				2020					2025					2030	
Pro	Leu	Asp	Glu	Pro	Ala	Glu	Leu	Gly	Leu	Arg	Glu	Arg	Val	Lys	Ala
				2035					2040					2045	
Ser	Val	Glu	His	Ile	Ser	Arg	Ile	Leu	Lys	Gly	Arg	Pro	Glu	Gly	Leu
				2050					2055					2060	

Glu Lys Glu Gly Pro Pro Arg Lys Lys Pro Gly Leu Ala Ser Phe Arg
 2065 2070 2075 2080
 Leu Ser Gly Leu Lys Ser Trp Asp Arg Ala Pro Thr Phe Leu Arg Glu
 2085 2090 2095
 Leu Ser Asp Glu Thr Val Val Leu Gly Gln Ser Val Thr Leu Ala Cys
 2100 2105 2110
 Gln Val Ser Ala Gln Pro Ala Ala Gln Ala Thr Trp Ser Lys Asp Gly
 2115 2120 2125
 Ala Pro Leu Glu Ser Ser Ser Arg Val Leu Ile Ser Ala Thr Leu Lys
 2130 2135 2140
 Asn Phe Gln Leu Leu Thr Ile Leu Val Val Val Ala Glu Asp Leu Gly
 2145 2150 2155 2160
 Val Tyr Thr Cys Ser Val Ser Asn Ala Leu Gly Thr Val Thr Thr
 2165 2170 2175
 Gly Val Leu Arg Lys Ala Glu Arg Pro Ser Ser Ser Pro Cys Pro Asp
 2180 2185 2190
 Ile Gly Glu Val Tyr Ala Asp Gly Val Leu Leu Val Trp Lys Pro Val
 2195 2200 2205
 Glu Ser Tyr Gly Pro Val Thr Tyr Ile Val Gln Cys Ser Leu Glu Gly
 2210 2215 2220
 Gly Ser Trp Thr Thr Leu Ala Ser Asp Ile Phe Asp Cys Cys Tyr Leu
 2225 2230 2235 2240
 Thr Ser Lys Leu Ser Arg Gly Gly Thr Tyr Thr Phe Arg Thr Ala Cys
 2245 2250 2255
 Val Ser Lys Ala Gly Met Gly Pro Tyr Ser Ser Pro Ser Glu Gln Val
 2260 2265 2270
 Leu Leu Gly Ala Pro Ser His Leu Ala Ser Glu Glu Glu Ser Gln Gly
 2275 2280 2285
 Arg Ser Ala Gln Pro Leu Pro Ser Thr Lys Thr Phe Ala Phe Gln Thr
 2290 2295 2300
 Gln Ile Gln Arg Gly Arg Phe Ser Val Val Arg Gln Cys Trp Glu Lys
 2305 2310 2315 2320
 Ala Ser Gly Arg Ala Leu Ala Ala Lys Ile Ile Pro Tyr His Pro Lys
 2325 2330 2335
 Asp Lys Thr Ala Val Leu Arg Glu Tyr Glu Ala Leu Lys Gly Leu Arg
 2340 2345 2350
 His Pro His Leu Ala Gln Leu His Ala Ala Tyr Leu Ser Pro Arg His
 2355 2360 2365
 Leu Val Leu Ile Leu Glu Leu Cys Ser Gly Pro Glu Leu Leu Pro Cys
 2370 2375 2380
 Leu Ala Glu Arg Ala Ser Tyr Ser Glu Ser Glu Val Lys Asp Tyr Leu
 2385 2390 2395 2400
 Trp Gln Met Leu Ser Ala Thr Gln Tyr Leu His Asn Gln His Ile Leu
 2405 2410 2415
 His Leu Asp Leu Arg Ser Glu Asn Met Ile Ile Thr Glu Tyr Asn Leu
 2420 2425 2430
 Leu Lys Val Val Asp Leu Gly Asn Ala Gln Ser Leu Ser Gln Glu Lys
 2435 2440 2445
 Val Leu Pro Ser Asp Lys Phe Lys Asp Tyr Leu Glu Thr Met Ala Pro
 2450 2455 2460
 Glu Leu Leu Glu Gly Gln Gly Ala Val Pro Gln Thr Asp Ile Trp Ala
 2465 2470 2475 2480
 Ile Gly Val Thr Ala Phe Ile Met Leu Ser Ala Glu Tyr Pro Val Ser
 2485 2490 2495
 Ser Glu Gly Ala Arg Asp Leu Gln Arg Gly Leu Arg Lys Gly Leu Val
 2500 2505 2510
 Arg Leu Ser Arg Cys Tyr Ala Gly Leu Ser Gly Gly Ala Val Ala Phe

2515	2520	2525
Leu Arg Ser Thr Leu Cys Ala Gln Pro Trp Gly Arg Pro Cys Ala Ser		
2530	2535	2540
Ser Cys Leu Gln Cys Pro Trp Leu Thr Glu Glu Gly Pro Ala Cys Ser		
2545	2550	2555
Arg Pro Ala Pro Val Thr Phe Pro Thr Ala Arg Leu Arg Val Phe Val		
	2565	2570
Arg Asn Arg Glu Lys Arg Arg Ala Leu Leu Tyr Lys Arg His Asn Leu		
2580	2585	2590
Ala Gln Val Arg		
2595		

<210> 7
 <211> 871
 <212> PRT
 <213> Homo sapiens

<400> 7

Met Gly Pro Gly Asp Ile Ser Leu Pro Gly Arg Pro Lys Pro Gly Pro		
1	5	10
Cys Ser Ser Pro Gly Ser Ala Ser Gln Ala Ser Ser Ser Gln Val Ser		
20	25	30
Ser Leu Arg Val Gly Ser Ser Gln Val Gly Thr Glu Pro Gly Pro Ser		
35	40	45
Leu Asp Ala Glu Gly Trp Thr Gln Glu Ala Glu Asp Leu Ser Asp Ser		
50	55	60
Thr Pro Thr Leu Gln Arg Pro Gln Glu Gln Ala Thr Met Arg Lys Phe		
65	70	75
Ser Leu Gly Gly Arg Gly Gly Tyr Ala Gly Val Ala Gly Tyr Gly Thr		
	85	90
Phe Ala Phe Gly Gly Asp Ala Gly Gly Met Leu Gly Gln Gly Pro Met		
100	105	110
Trp Ala Arg Ile Ala Trp Ala Val Ser Gln Ser Glu Glu Glu Glu Gln		
115	120	125
Glu Glu Ala Arg Ala Glu Ser Gln Ser Glu Glu Gln Gln Glu Ala Arg		
130	135	140
Ala Glu Ser Pro Leu Pro Gln Val Ser Ala Arg Pro Val Pro Glu Val		
145	150	155
Gly Arg Ala Pro Thr Arg Ser Ser Pro Glu Pro Thr Pro Trp Glu Asp		
	165	170
Ile Gly Gln Val Ser Leu Val Gln Ile Arg Asp Leu Ser Gly Asp Ala		
180	185	190
Glu Ala Ala Asp Thr Ile Ser Leu Asp Ile Ser Glu Val Asp Pro Ala		
195	200	205
Tyr Leu Asn Leu Ser Asp Leu Tyr Asp Ile Lys Tyr Leu Pro Phe Glu		
210	215	220
Phe Met Ile Phe Arg Lys Val Pro Lys Ser Ala Gln Pro Glu Pro Pro		
225	230	235
Ser Pro Met Ala Glu Glu Glu Leu Ala Glu Phe Pro Glu Pro Thr Trp		

				245				250				255				
Pro	Trp	Pro	Gly	Glu	Leu	Gly	Pro	His	Ala	Gly	Leu	Glu	Ile	Thr	Glu	
				260					265					270		
Glu	Ser	Glu	Asp	Val	Asp	Ala	Leu	Leu	Ala	Glu	Ala	Ala	Val	Gly	Arg	
				275					280					285		
Lys	Arg	Lys	Trp	Ser	Ser	Pro	Ser	Arg	Ser	Leu	Phe	His	Phe	Pro	Gly	
				290					295					300		
Arg	His	Leu	Pro	Leu	Asp	Glu	Pro	Ala	Glu	Leu	Gly	Leu	Arg	Glu	Arg	
305					310					315					320	
Val	Lys	Ala	Ser	Val	Glu	His	Ile	Ser	Arg	Ile	Leu	Lys	Gly	Arg	Pro	
				325					330					335		
Glu	Gly	Leu	Glu	Lys	Glu	Gly	Pro	Pro	Arg	Lys	Lys	Pro	Gly	Leu	Ala	
				340					345					350		
Ser	Phe	Arg	Leu	Ser	Gly	Leu	Lys	Ser	Trp	Asp	Arg	Ala	Pro	Thr	Phe	
				355					360					365		
Leu	Arg	Glu	Leu	Ser	Asp	Glu	Thr	Val	Val	Leu	Gly	Gln	Ser	Val	Thr	
				370					375					380		
Leu	Ala	Cys	Gln	Val	Ser	Ala	Gln	Pro	Ala	Ala	Gln	Ala	Thr	Trp	Ser	
385					390					395					400	
Lys	Asp	Gly	Ala	Pro	Leu	Glu	Ser	Ser	Ser	Arg	Val	Leu	Ile	Ser	Ala	
				405					410					415		
Thr	Leu	Lys	Asn	Phe	Gln	Leu	Leu	Thr	Ile	Leu	Val	Val	Val	Ala	Glu	
				420					425					430		
Asp	Leu	Gly	Val	Tyr	Thr	Cys	Ser	Val	Ser	Asn	Ala	Leu	Gly	Thr	Val	
				435					440					445		
Thr	Thr	Thr	Gly	Val	Leu	Arg	Lys	Ala	Glu	Arg	Pro	Ser	Ser	Ser	Pro	
				450					455					460		
Cys	Pro	Asp	Ile	Gly	Glu	Val	Tyr	Ala	Asp	Gly	Val	Leu	Leu	Val	Trp	
465					470					475					480	
Lys	Pro	Val	Glu	Ser	Tyr	Gly	Pro	Val	Thr	Tyr	Ile	Val	Gln	Cys	Ser	
				485					490					495		
Leu	Glu	Gly	Gly	Ser	Trp	Thr	Thr	Leu	Ala	Ser	Asp	Ile	Phe	Asp	Cys	
				500					505					510		
Cys	Tyr	Leu	Thr	Ser	Lys	Leu	Ser	Arg	Gly	Gly	Thr	Tyr	Thr	Phe	Arg	
				515					520					525		
Thr	Ala	Cys	Val	Ser	Lys	Ala	Gly	Met	Gly	Pro	Tyr	Ser	Ser	Pro	Ser	
				530					535					540		
Glu	Gln	Val	Leu	Leu	Gly	Gly	Pro	Ser	His	Leu	Ala	Ser	Glu	Glu	Glu	
545					550					555					560	
Ser	Gln	Gly	Arg	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Thr	Lys	Thr	Phe	Ala	
				565					570					575		
Phe	Gln	Thr	Gln	Ile	Gln	Arg	Gly	Arg	Phe	Ser	Val	Val	Arg	Gln	Cys	
				580					585					590		
Trp	Glu	Lys	Ala	Ser	Gly	Arg	Ala	Leu	Ala	Ala	Lys	Ile	Ile	Pro	Tyr	
				595					600					605		
His	Pro	Lys	Asp	Lys	Thr	Ala	Val	Leu	Arg	Glu	Tyr	Glu	Ala	Leu	Lys	
				610					615					620		
Gly	Leu	Arg	His	Pro	His	Leu	Ala	Gln	Leu	His	Ala	Ala	Tyr	Leu	Ser	
625					630					635					640	
Pro	Arg	His	Leu	Val	Leu	Ile	Leu	Glu	Leu	Cys	Ser	Gly	Pro	Glu	Leu	
				645					650					655		
Leu	Pro	Cys														

Tyr Asn Leu Leu Lys Val Val Asp Leu Gly Asn Ala Gln Ser Leu Ser
 705 710 715 720
 Gln Glu Lys Val Leu Pro Ser Asp Lys Phe Lys Asp Tyr Leu Glu Thr
 725 730 735
 Met Ala Pro Glu Leu Leu Glu Gly Gln Gly Ala Val Pro Gln Thr Asp
 740 745 750
 Ile Trp Ala Ile Gly Val Thr Ala Phe Ile Met Leu Ser Ala Glu Tyr
 755 760 765
 Pro Val Ser Ser Glu Gly Ala Arg Asp Leu Gln Arg Gly Leu Arg Lys
 770 775 780
 Gly Leu Val Arg Leu Ser Arg Cys Tyr Ala Gly Leu Ser Gly Gly Ala
 785 790 795 800
 Val Ala Phe Leu Arg Ser Thr Leu Cys Ala Gln Pro Trp Gly Arg Pro
 805 810 815
 Cys Ala Ser Ser Cys Leu Gln Cys Pro Trp Leu Thr Glu Glu Gly Pro
 820 825 830
 Ala Cys Ser Arg Pro Ala Pro Val Thr Phe Pro Thr Ala Arg Leu Arg
 835 840 845
 Val Phe Val Arg Asn Arg Glu Lys Arg Arg Ala Leu Leu Tyr Lys Arg
 850 855 860
 His Asn Leu Ala Gln Val Arg
 865 870

<210> 8

<211> 548

<212> PRT

<213> Rattus norvegicus

<400> 8

Met Ala His Ile Ser Arg Ile Leu Lys Gly Lys Pro Glu Gly Pro Glu
 1 5 10 15
 Lys Glu Gly Pro Pro Arg Lys Lys Ala Gly Leu Ala Ser Phe Arg Leu
 20 25 30
 Ser Gly Leu Lys Gly Arg Asp Gln Ala Pro Ser Phe Leu Arg Glu Leu
 35 40 45
 Ser Asp Glu Ala Val Val Leu Gly Gln Ser Val Thr Leu Ala Cys Gln
 50 55 60
 Val Leu Ala Gln Pro Thr Ala Gln Ala Thr Trp Ser Lys Asp Gly Ala
 65 70 75 80
 Leu Leu Glu Ser Ser Gly His Leu Leu Ile Ser Ser Thr Leu Lys Asn
 85 90 95
 Phe Gln Leu Leu Thr Ile Leu Val Val Thr Glu Glu Asp Leu Gly Thr
 100 105 110
 Tyr Thr Cys Cys Val Ser Asn Pro Leu Gly Thr Ala Val Thr Thr Gly
 115 120 125
 Val Leu Arg Lys Ala Glu Arg Pro Ser Ser Ser Pro Arg Pro Glu Val
 130 135 140
 Gly Glu Leu Tyr Thr Asp Ala Val Leu Leu Val Trp Lys Pro Val Glu
 145 150 155 160
 Ser Tyr Gly Pro Val Thr Tyr Ile Val Gln Cys Cys Ile Glu Gly Gly
 165 170 175
 Ser Trp Thr Thr Leu Ala Ser Asp Ile Ser Asp Cys Cys Tyr Leu Thr
 180 185 190
 Gly Lys Leu Pro Arg Gly Gly Met Tyr Thr Phe Arg Thr Ala Cys Val
 195 200 205
 Ser Lys Ala Gly Met Gly Pro Tyr Ser Ser Pro Ser Glu Gln Val Leu
 210 215 220

Leu Gly Gly Pro Asn His Leu Ala Ser Glu Glu Glu Ser Ser Arg Gly
 225 230 235 240
 Arg Pro Ala Gln Leu Leu Pro Ser Thr Lys Thr Phe Ala Phe Gln Thr
 245 250 255
 Gln Ile Arg Arg Gly Arg Phe Ser Val Val Arg Gln Cys Arg Glu Lys
 260 265 270
 Ala Ser Gly Arg Ala Leu Ala Ala Lys Ile Val Pro Tyr Gln Pro Glu
 275 280 285
 Asp Lys Thr Thr Val Leu Arg Glu Tyr Glu Ala Leu Lys Arg Leu His
 290 295 300
 His Pro His Leu Ala Gln Leu His Ala Ala Tyr Leu Ser Pro Arg His
 305 310 315 320
 Leu Val Leu Ile Leu Glu Leu Cys Ser Gly Pro Glu Leu Leu Pro Ser
 325 330 335
 Leu Ala Glu Arg Asp Ser Tyr Ser Glu Ser Asp Val Lys Asp Tyr Leu
 340 345 350
 Trp Gln Met Leu Ser Ala Thr Gln Tyr Leu His Ala Gln His Ile Leu
 355 360 365
 His Leu Asp Leu Arg Ser Glu Asn Met Met Val Thr Glu Tyr Asn Leu
 370 375 380
 Leu Lys Val Ile Asp Leu Gly Asn Ala Gln Ser Leu Ser Gln Glu Lys
 385 390 395 400
 Val Pro Pro Pro Glu Asn Phe Lys Asp Tyr Leu Glu Thr Met Ala Pro
 405 410 415
 Glu Leu Leu Glu Gly Gln Gly Ala Val Pro Gln Thr Asp Ile Trp Ala
 420 425 430
 Ile Gly Val Thr Ala Phe Ile Met Leu Ser Gly Glu Tyr Pro Val Ser
 435 440 445
 Ser Glu Gly Thr Arg Asp Leu Gln Lys Gly Leu Arg Lys Gly Leu Ile
 450 455 460
 Gln Leu Ser Arg Cys Tyr Ala Gly Leu Ser Gly Gly Ala Val Ala Phe
 465 470 475 480
 Leu Gln Ser Ser Leu Cys Ala Arg Pro Trp Gly Arg Pro Cys Ala Ser
 485 490 495
 Thr Cys Leu Gln Cys Gly Trp Leu Thr Glu Glu Gly Pro Thr Gly Ser
 500 505 510
 Arg Pro Thr Pro Val Thr Phe Pro Thr Ala Arg Leu Arg Ala Phe Val
 515 520 525
 Arg Glu Arg Glu Lys Arg Arg Ala Leu Leu Tyr Lys Lys His Asn Leu
 530 535 540
 Ala Gln Val Arg
 545

<210> 9
 <211> 548
 <212> PRT
 <213> Mus musculus

<400> 9
 Met Ala His Ile Ser Arg Ile Leu Lys Gly Arg Pro Glu Gly Pro Glu
 1 5 10 15
 Arg Glu Gly Pro Pro Arg Lys Lys Ala Gly Leu Ala Ser Phe Arg Leu

				20					25					30			
Ser	Gly	Leu	Lys	Gly	Arg	Asp	Gln	Ala	Pro	Ser	Phe	Leu	Arg	Glu	Leu		
		35					40					45					
Ser	Asp	Glu	Ala	Val	Val	Leu	Gly	Gln	Ser	Val	Thr	Leu	Ala	Cys	Gln		
	50					55					60						
Val	Leu	Ala	Gln	Pro	Thr	Ala	Gln	Ala	Thr	Trp	Ser	Lys	Asp	Gly	Val		
65					70					75					80		
Leu	Leu	Glu	Ser	Ser	Gly	His	Leu	Leu	Ile	Ser	Ser	Thr	Leu	Lys	Asn		
				85					90					95			
Phe	Gln	Leu	Leu	Thr	Ile	Leu	Val	Val	Lys	Glu	Glu	Asp	Leu	Gly	Thr		
			100					105					110				
Tyr	Thr	Cys	Cys	Val	Ser	Asn	Pro	Leu	Gly	Thr	Ala	Val	Thr	Thr	Gly		
		115					120					125					
Val	Leu	Arg	Lys	Ala	Glu	Arg	Pro	Ser	Ser	Ser	Pro	Arg	Pro	Glu	Val		
	130					135					140						
Gly	Glu	Leu	Tyr	Lys	Asp	Ala	Val	Leu	Leu	Val	Trp	Lys	Pro	Val	Glu		
145					150					155					160		
Ser	Cys	Gly	Pro	Val	Thr	Tyr	Ile	Val	Gln	Cys	Cys	Ile	Glu	Gly	Gly		
				165					170					175			
Ser	Trp	Thr	Thr	Leu	Ala	Ser	Asp	Ile	Ser	Asp	Cys	Cys	Tyr	Leu	Thr		
			180					185					190				
Gly	Lys	Leu	Ser	Arg	Gly	Gly	Met	Tyr	Ile	Phe	Arg	Thr	Ala	Cys	Val		
		195					200					205					
Ser	Lys	Ala	Gly	Met	Gly	Pro	Tyr	Ser	Ser	Pro	Ser	Glu	Gln	Val	Leu		
	210					215					220						
Leu	Gly	Gly	Pro	Asn	His	Leu	Ala	Ser	Glu	Glu	Glu	Ser	Ser	Arg	Gly		
225					230					235					240		
Arg	Pro	Ala	Gln	Leu	Leu	Pro	Ser	Thr	Lys	Thr	Phe	Ala	Phe	Gln	Met		
				245					250					255			
Gln	Ile	Arg	Arg	Gly	Arg	Phe	Ser	Val	Val	Arg	Gln	Cys	Arg	Glu	Lys		
			260					265					270				
Ala	Ser	Gly	Arg	Ala	Leu	Ala	Ala	Lys	Ile	Val	Pro	Tyr	Gln	Pro	Glu		
		275					280					285					
Asp	Lys	Thr	Ala	Val	Leu	Arg	Glu	Tyr	Glu	Ala	Leu	Lys	Arg	Leu	His		
	290					295					300						
His	Pro	His	Leu	Ala	Gln	Leu	His	Ala	Ala	Tyr	Leu	Ser	Pro	Arg	His		
305					310					315					320		
Leu	Val	Leu	Ile	Leu	Glu	Leu	Cys	Ser	Gly	Pro	Glu	Leu	Leu	Pro	Ser		
				325					330					335			
Leu	Ala	Glu	Arg	Glu	Ser	Tyr	Ser	Glu	Ser	Asp	Val	Lys	Asp	Tyr	Leu		
			340					345					350				

Leu Gln Ser Ser Leu Cys Ala Gln Pro Trp Gly Arg Pro Cys Ala Ser
485 490 495
Thr Cys Leu Gln Cys Gly Trp Leu Thr Glu Glu Gly Pro Thr Gly Ser
500 505 510
Arg Pro Thr Pro Val Thr Phe Pro Thr Val Arg Leu Arg Ala Phe Val
515 520 525
Arg Glu Arg Glu Lys Arg Arg Ala Leu Leu Tyr Lys Lys His Asn Leu
530 535 540
Ala Gln Val Arg
545

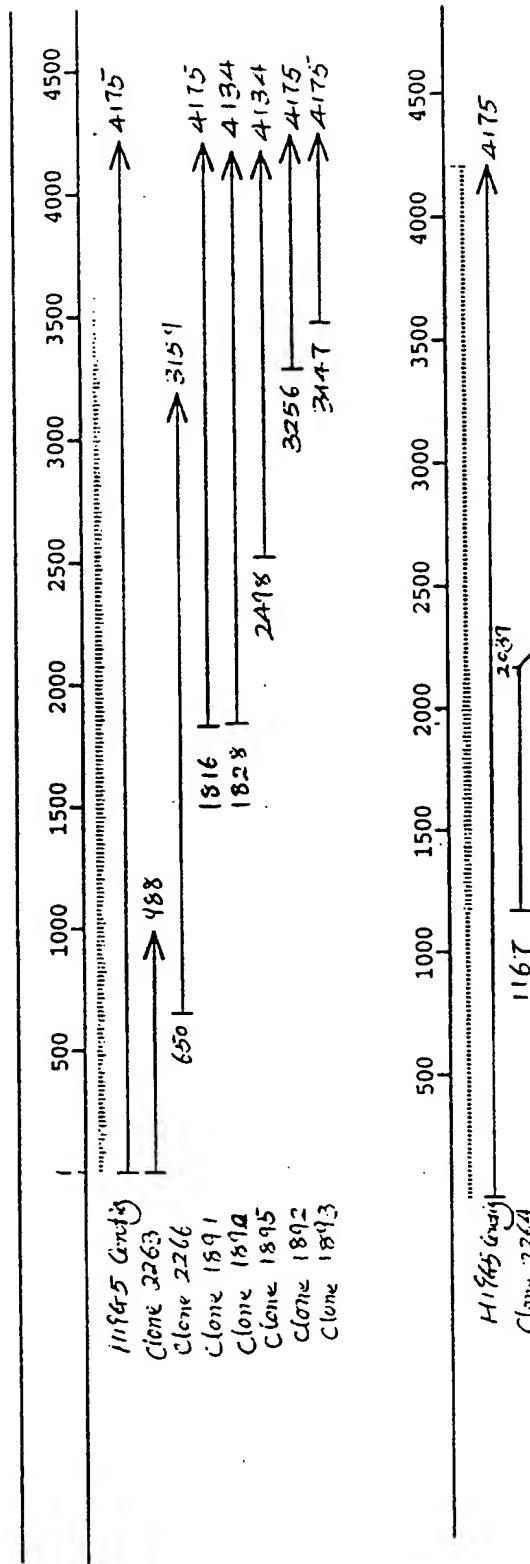


FIG. 1

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.
Monday, April 3, 2000 5:11 PM

Page 1

M A		Majority			
		10	20	30	40
1	M G P G D I S L P G R P K P G P C S S P G S A S Q A S S S Q V S S L R V G S S Q	H19G5-F1.pep			
1	M A	R19G5-S.pep			
1	M A	M19G5-S.pep			

		Majority			
		50	60	70	80
41	V G T E P G P S L D A E G W T Q E A E D L S D S T P T L Q R P Q E Q A T M R K F	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		90	100	110	120
81	S L G G R G G Y A G V A G Y G T F A F G G D A G G M L G Q G P M W A R I A W A V	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		130	140	150	160
121	S Q S E E E E Q E E A R A E S Q S E E Q Q E A R A E S P L P Q V S A R P V P E V	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		170	180	190	200
161	G R A P T R S S P E P T P W E D I G Q V S L V Q I R D L S G D A E A A D T I S L	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		210	220	230	240
201	D I S E V D P A Y L N L S D L Y D I K Y L P F E F M I F R K V P K S A Q P E P P	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		250	260	270	280
241	S P M A E E E L A E F P E P T W P W P G E L G P H A G L E I T E E S E D V D A L	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

		Majority			
		290	300	310	320
281	L A E A A V G R K R K W S S P S R S L F H F P G R H L P L D E P A E L G L R E R	H19G5-F1.pep			
3	-----	R19G5-S.pep			
3	-----	M19G5-S.pep			

FIG. 2

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.
Monday, April 3, 2000 5:11 PM

Page 2

```

- - - - - H I S R I L K G R P E G P E K E G P P R K K A G L A S F R L S G L K Majority
              330              340              350              360
321 VKASVE H I S R I L K G R P E G L E K E G P P R K K P G L A S F R L S G L K H19G5-F1.pep
3  - - - - - H I S R I L K G K P E G P E K E G P P R K K A G L A S F R L S G L K R19G5-S.pep
3  - - - - - H I S R I L K G R P E G P E R E G P P R K K A G L A S F R L S G L K M19G5-S.pep

GRDQAPSFLRELSDEAVVLGQSVTLACQVLAQPTAQATWS Majority
              370              380              390              400
361 SWDRAP T F L R E L S D E T V V L G Q S V T L A C Q V S A Q P A A Q A T W S H19G5-F1.pep
37 GRDQAPSFLRELSDEAVVLGQSVTLACQVLAQPTAQATWS R19G5-S.pep
37 GRDQAPSFLRELSDEAVVLGQSVTLACQVLAQPTAQATWS M19G5-S.pep

KDGA L L E S S G H L L I S S T L K N F Q L L T I L V V X E E D L G T Y T C C Majority
              410              420              430              440
401 KDGA P L E S S S R V L I S A T L K N F Q L L T I L V V V A E D L G V Y T C S H19G5-F1.pep
77 KDGA L L E S S G H L L I S S T L K N F Q L L T I L V V T E E D L G T Y T C C R19G5-S.pep
77 K D G V L L E S S G H L L I S S T L K N F Q L L T I L V V K E E D L G T Y T C C M19G5-S.pep

VSNPLGTAVTTGVLRKAERPSSSPRPEVGELYXDAVLLVW Majority
              450              460              470              480
441 VSN A L G T V T T T G V L R K A E R P S S S P C P D I G E V V A D G V L L V W H19G5-F1.pep
117 VSNPLGTAVTTGVLRKAERPSSSPRPEVGELYTDAVLLVW R19G5-S.pep
117 VSNPLGTAVTTGVLRKAERPSSSPRPEVGELYKDAVLLVW M19G5-S.pep

KPVESYGPVTYIVQCCIEGGSWTTLASDISDCCYLTGKLS Majority
              490              500              510              520
481 KPVESYGPVTYIVQCC S L E G G S W T T L A S D I F D C C Y L T S K L S H19G5-F1.pep
157 KPVESYGPVTYIVQCCIEGGSWTTLASDISDCCYLTGKLP R19G5-S.pep
157 KPVES C G P V T Y I V Q C C I E G G S W T T L A S D I S D C C Y L T G K L S M19G5-S.pep

RGGMYTFRTACVSKAGMGPHYSSPSEQVLLGGPNHLASEEE Majority
              530              540              550              560
521 RGG T Y T F R T A C V S K A G M G P Y S S P S E Q V L L G G P N H L A S E E E H19G5-F1.pep
197 RGGMYTFRTACVSKAGMGPHYSSPSEQVLLGGPNHLASEEE R19G5-S.pep
197 RGGMY I T F R T A C V S K A G M G P Y S S P S E Q V L L G G P N H L A S E E E M19G5-S.pep

SSRGRPAQLLPSTKTFAFQTQIRRGFRFSVVRQCREKASGR Majority
              570              580              590              600
561 S - Q G R S A Q P L P S T K T F A F Q T Q I Q R G R F S V V R Q C W E K A S G R H19G5-F1.pep
237 SSRGRPAQLLPSTKTFAFQTQIRRGFRFSVVRQCREKASGR R19G5-S.pep
237 SSRGRPAQLLPSTKTFAFOMQIRRGFRFSVVRQCREKASGR M19G5-S.pep

ALAAKIVPYQPEDKTAVLREYEALKRLHHPHLAQLHAAYL Majority
              610              620              630              640
600 ALAAKI I P Y H P K D K T A V L R E Y E A L K G L R H P H L A Q L H A A Y L H19G5-F1.pep
277 ALAAKIVPYQPEDKT T V L R E Y E A L K R L H H P H L A Q L H A A Y L R19G5-S.pep
277 ALAAKIVPYQPEDKTAVLREYEALKRLHHPHLAQLHAAYL M19G5-S.pep

```

Alignment Report of 19G5 align, using Clustal method with PAM250 residue weight table.
Monday, April 3, 2000 5:15 PM

Page 3

S P R H L V L I L E L C S G P E L L P S L A E R X S Y S E S D V K D Y L W Q M L																																Majority
650660670680																																
640	S P R H L V L I L E L C S G P E L L P C L A E R A I S Y S E S E V K D Y L W Q M L																															H19G5-F1.pep
317	S P R H L V L I L E L C S G P E L L P S L A E R D S Y S E S D V K D Y L W Q M L																															R19G5-S.pep
317	S P R H L V L I L E L C S G P E L L P S L A E R E S Y S E S D V K D Y L W Q M L																															M19G5-S.pep
S A T Q Y L H A Q H I L H L D L R S E N M M V T E Y N L L K V I D L G N A Q S L																																Majority
690700710720																																
680	S A T Q Y L H N Q H I L H L D L R S E N M I I I T E Y N L L K V V I D L G N A Q S L																															H19G5-F1.pep
357	S A T Q Y L H A Q H I L H L D L R S E N M M V T E Y N L L K V I D L G N A Q S L																															R19G5-S.pep
357	S A T O Y L H A Q H I L H L D L R S E N M M V T E Y N L L K V I D L G N A Q S L																															M19G5-S.pep
S Q E K V P P P E N F K D Y L E T M A P E L L E G Q G A V P Q T D I W A I G V T																																Majority
730740750760																																
720	S Q E K V L P S D K F K D Y L E T M A P E L L E G Q G A V P Q T D I W A I G V T																															H19G5-F1.pep
397	S Q E K V P P P E N F K D Y L E T M A P E L L E G Q G A V P Q T D I W A I G V T																															R19G5-S.pep
397	D Q E K V P A P E N F K D Y L E T M A P E L L E G Q G A V P Q T D I W A I G V T																															M19G5-S.pep
A F I M L S G E Y P V S S E G T R D L Q K G L R K G L I R L S R C Y A G L S G G																																Majority
770780790800																																
760	A F I M L S A E Y P V S S E G A R D L Q R G L R K G L V R L S R C Y A G L S G G																															H19G5-F1.pep
437	A F I M L S G E Y P V S S E G T R D L Q K G L R K G L I Q L S R C Y A G L S G G																															R19G5-S.pep
437	A F I M L S G E Y P E S S E G T R D L Q K G L R K G L I R L S R C Y A G L S G G																															M19G5-S.pep
A V A F L Q S S L C A Q P W G R P C A S T C L Q C G W L T E E G P T G S R P T P																																Majority
810820830840																																
800	A V A F L R S T L C A Q P W G R P C A S S C L Q C P W L T E E G P A C S R P A P																															H19G5-F1.pep
477	A V A F L Q S S L C A R P W G R P C A S T C L Q C G W L T E E G P T G S R P T P																															R19G5-S.pep
477	A V A F L Q S S L C A Q P W G R P C A S T C L Q C G W L T E E G P T G S R P T P																															M19G5-S.pep
V T F P T A R L R A F V R E R E K R R A L L Y K K H N L A Q V R																																Majority
850860870																																
840	V T F P T A R L R V F V R N R E K R R A L L Y K R H N L A Q V R																															H19G5-F1.pep
517	V T F P T A R L R A F V R E R E K R R A L L Y K K H N L A Q V R																															R19G5-S.pep
517	V T F P T V R L R A F V R E R E K R R A L L Y K K H N L A Q V R																															M19G5-S.pep

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Human H19C5 Gene Structure

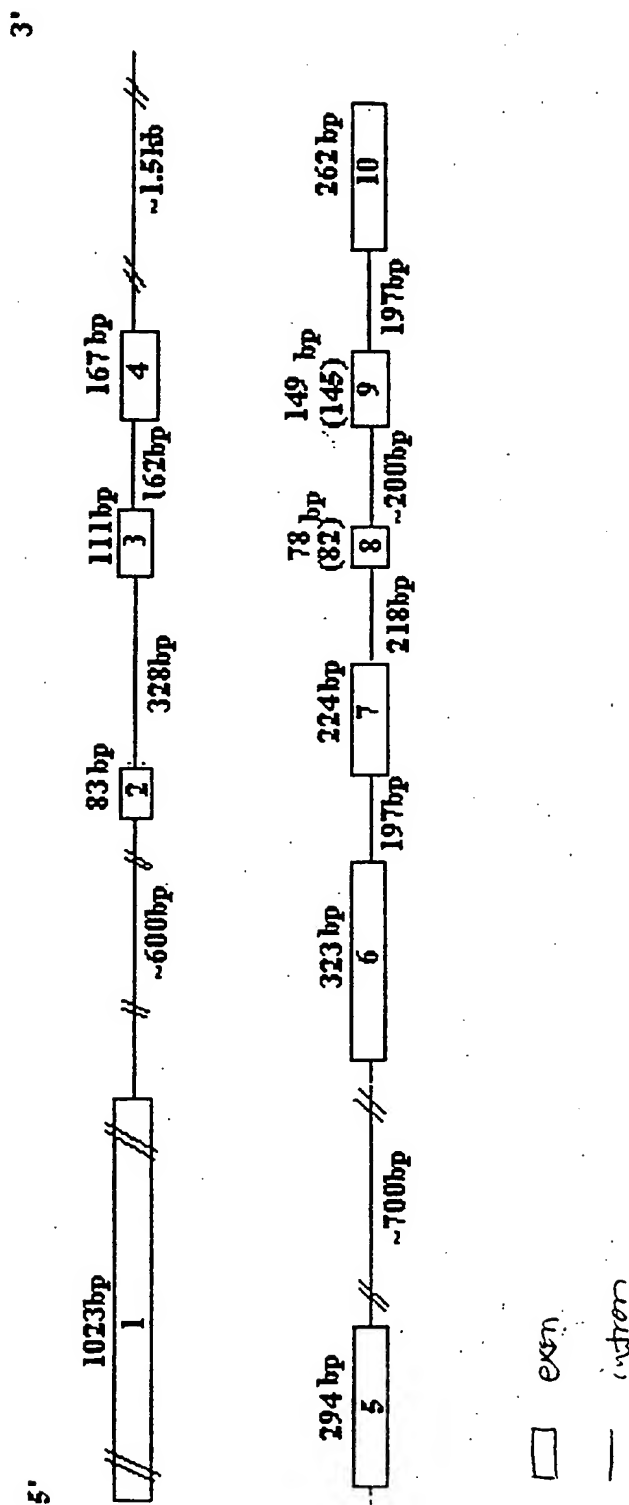


FIG. 3

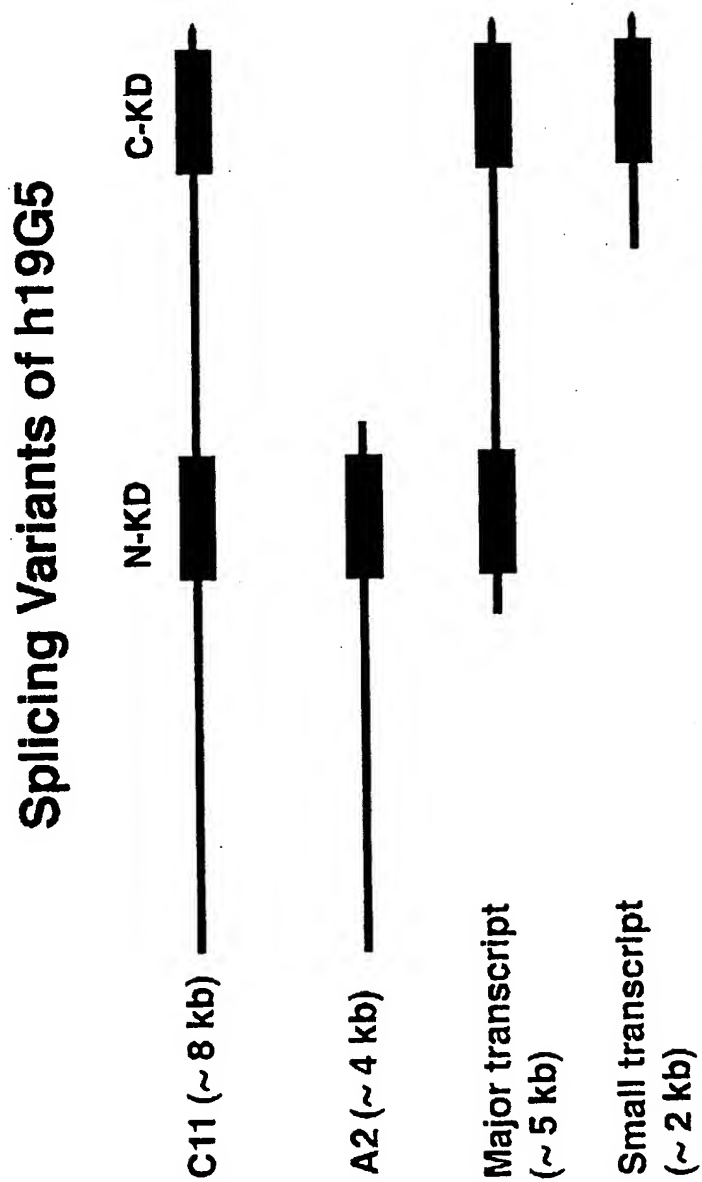


FIG. 4

Comparison of 19G5 and Trio Protein Structures

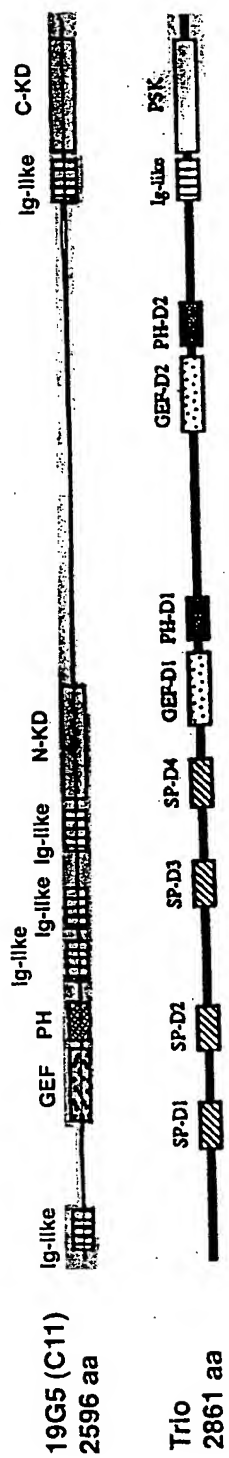


FIG. 5

Sequence Comparison of 19G5 , Trio, and MLCK Kinase Domains

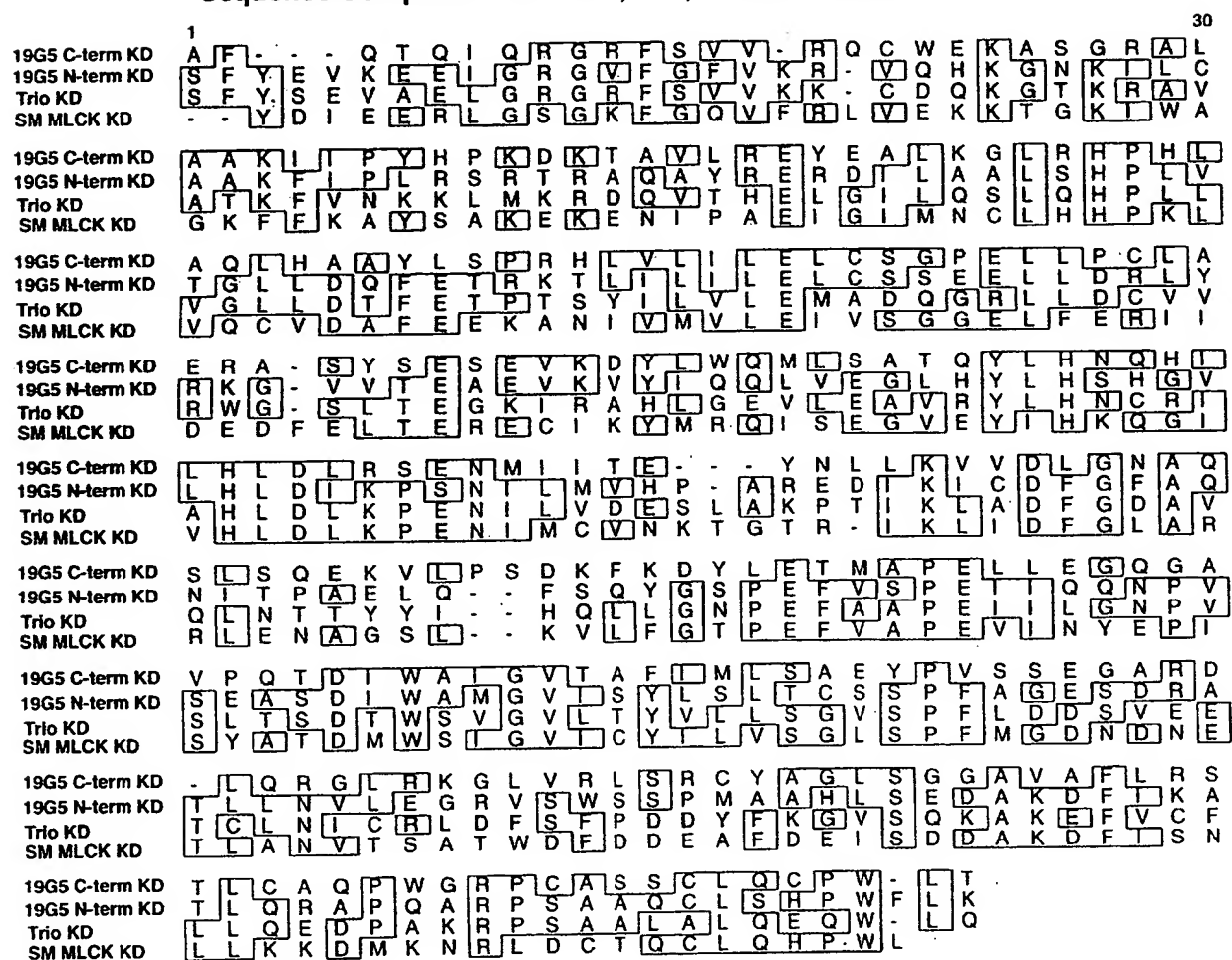
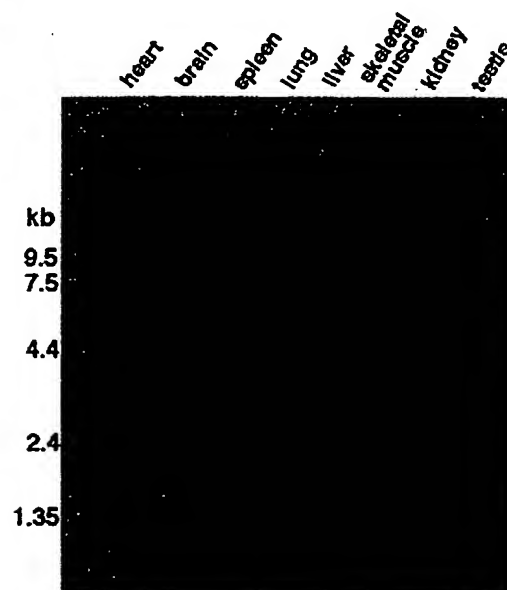
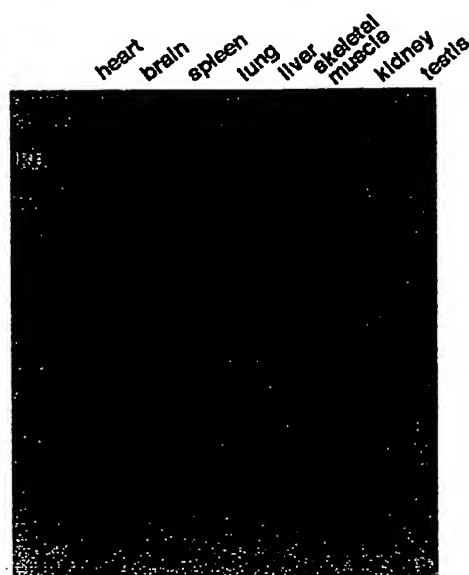


FIG. 6

Tissue distribution of Rat H19G5 kinase**Rat MTN Blot Probed with R19G5****Rat MTN Blot Probed with beta-Actin**

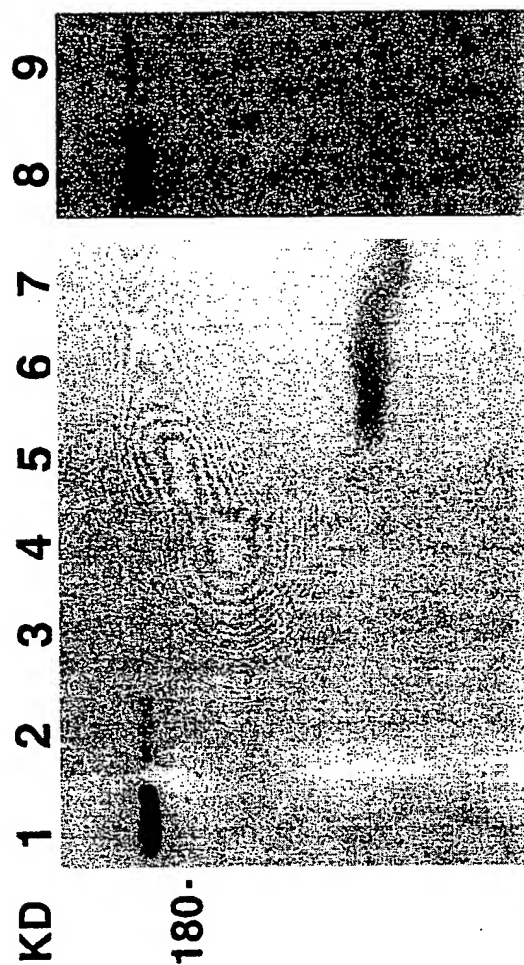
Human MTN Blot I Probed with H19G5



**Genomic Southern Blot with
H19G5 3917/3886 fragment as Probe**



H19G5 interaction with small G proteins



- | | |
|-------------------------|----------------------------|
| 1. H19G5/293EBNA lysate | 5. GST-Cdc42/GTP-gammaS |
| 2. GST-Cdc42 | 6. GST-Rac1/GTP-gammaS |
| 3. GST-Rac1 | 7. GST-RhoA/GTP-gammaS |
| 4. GST-RhoA | 8. His-tagged Cdc42 |
| | 9. Boiled His-tagged Cdc42 |

19G5-GFP Proteins' Localization In C2C12 Myoblast

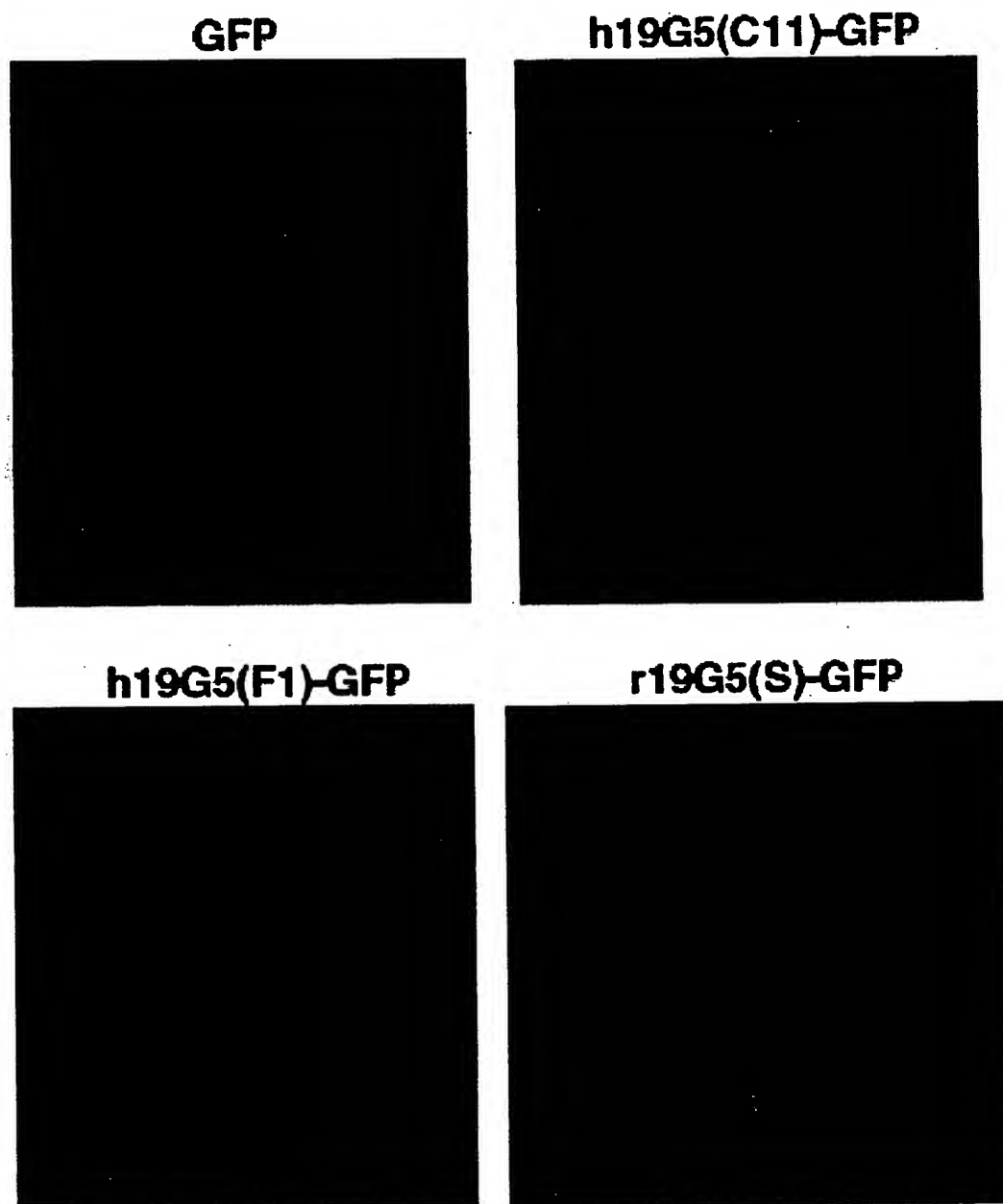


FIG. 12

C2C12 Myoblast Differentiation

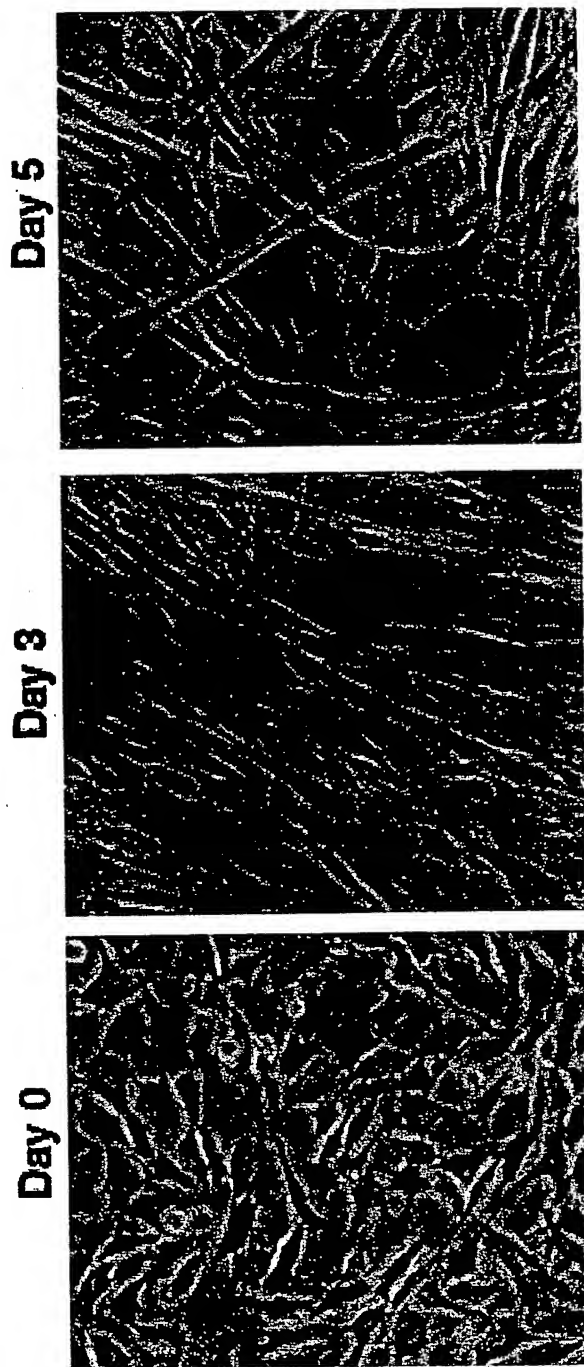


FIG. 13
15/18

Myogenin Induction During C2C12 Cell Differentiation

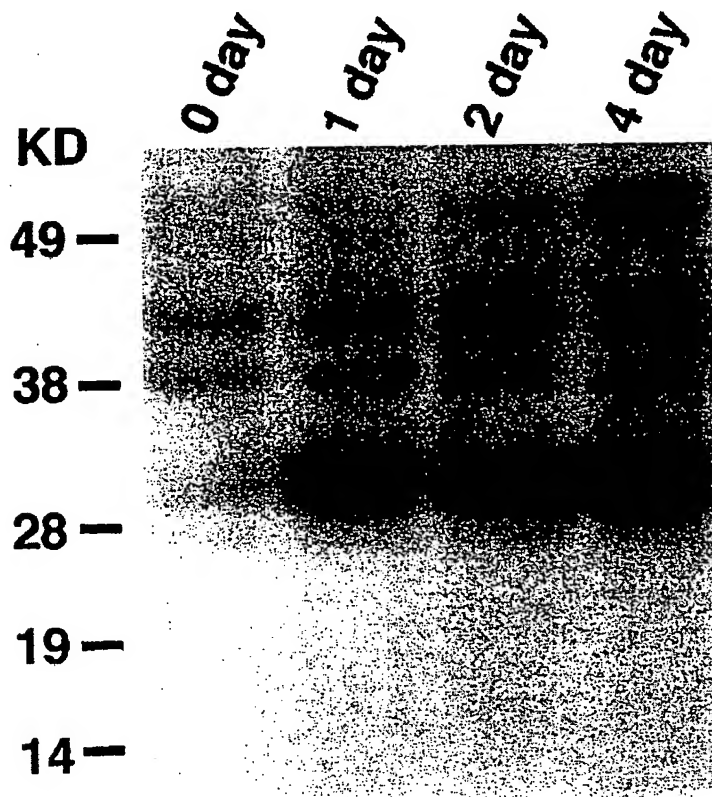


FIG. 14

19G5 Expression During C1C12 Myoblast Differentiation

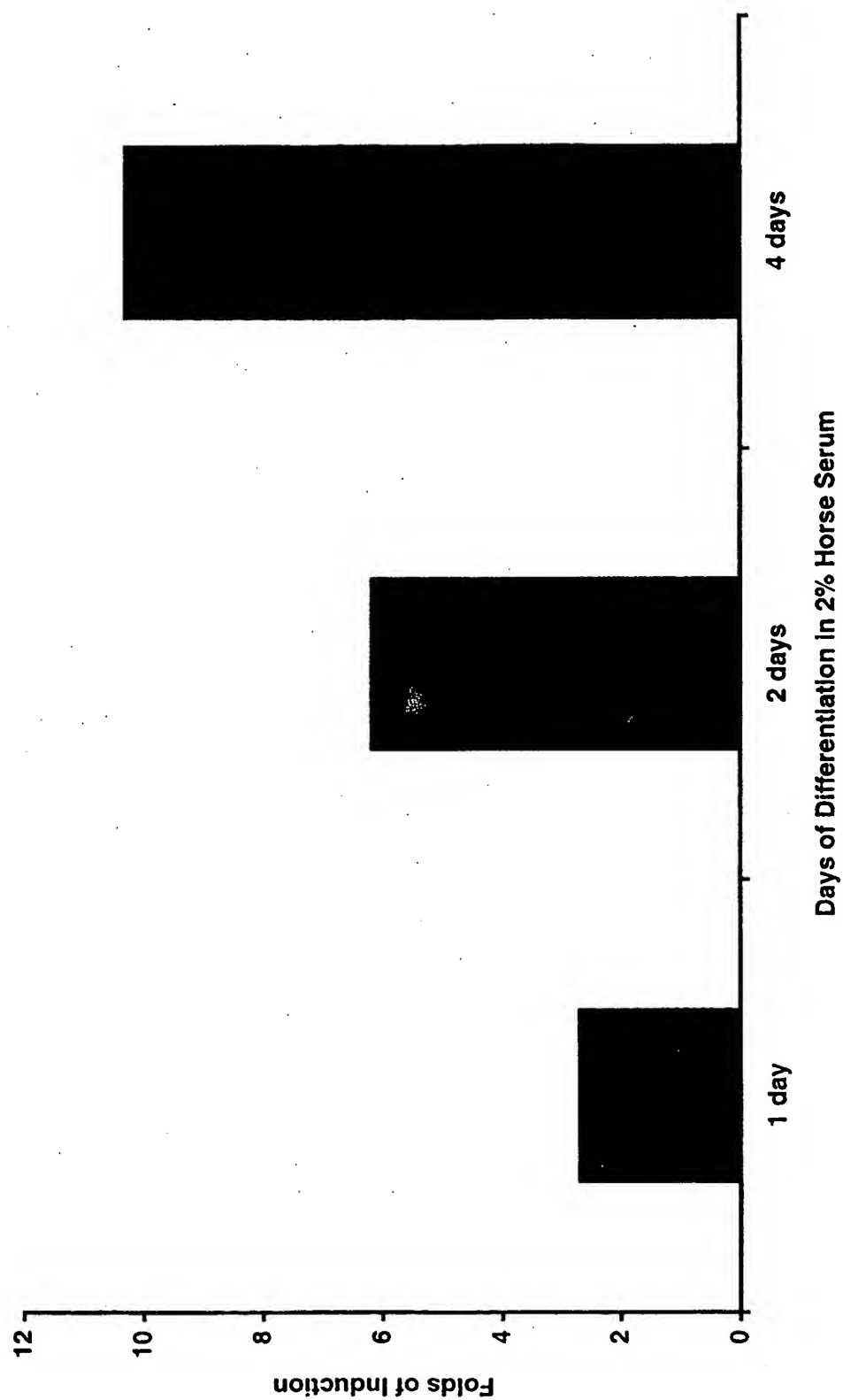


FIG. 15
17/18

TGF beta Inhibits 19G5 Expression in C2C12 Cells

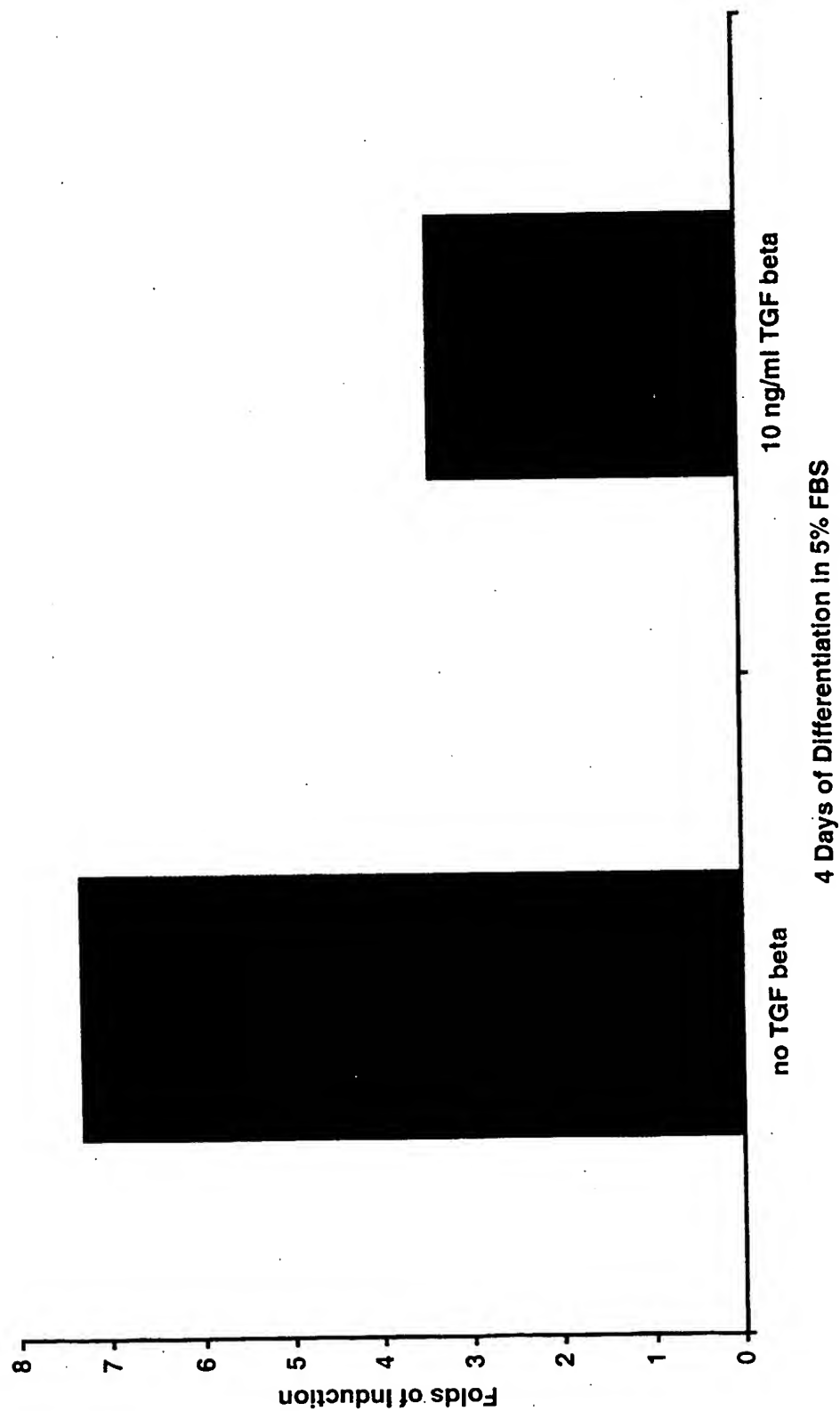


FIG. 16
18/18

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/09488

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C07K16/18 C12N15/11 G01N33/68
A61K38/17 A61K39/395 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WAYE M. M. Y. ET AL.: "Gene expression of adult human heart as revealed by random sequencing of a cDNA library." EMBL DATABASE ACCESSION NUMBER R45853, 26 May 1995 (1995-05-26), XP002143928 abstract	13-15
X	"The Genexpress cDNA program." EMBL DATABASE ACCESSION NUMBER Z19064, 15 December 1992 (1992-12-15), XP002143929 abstract	13-15



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

31 July 2000

Date of mailing of the international search report

10/08/2000

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040. Tx. 31 651 epo nl.
Fax: (+31-70) 340-3016

Authorized officer

Mandl. B

INTERNATIONAL SEARCH REPORT

Int. Patent Application No
PCT/US 00/09488

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DEBANT A. ET AL.: "The multidomain protein Trio binds the LAR transmembrane tyrosine phosphatase, contains a protein kinase domain, and has separate rac-specific and rho-specific guanine nucleotide exchange factor domains." PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 93, no. 11, 1996, pages 5466-5471, XP002143930 1996 ISSN: 0027-8424 the whole document -----</p>	1-37

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☒ **BLACK BORDERS**

☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

☐ **FADED TEXT OR DRAWING**

☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**

☐ **SKEWED/SLANTED IMAGES**

☒ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**

☐ **GRAY SCALE DOCUMENTS**

☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**

☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.